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THE FACE BLANK (USPTO)

GenCore version 5.1.4.p5.4578
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OM nucleic - nucleic search, using sw model

Run on: May 15, 2003, 19:37:55 ; Search time 1730 Seconds
(without alignments)
8032.213 Million cell updates/sec

Title: US-10-031-403-2

Perfect score: 858
Sequence: 1 aatcccgatccctgcgcgc.....aggactgcgcgattcccaaa 858

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

EST:
1: em_estba:*
2: em_esthum:*
3: em_estlin:*
4: em_estm:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hlc:*
9: gb_est1:*
10: gb_est2:*
11: gb_hlc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rtd:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	761.4	88.7	867	12	BG697492
2	750.8	87.5	819	12	BG680086
3	737.2	85.9	830	12	BG743203
4	715.4	83.4	976	12	BG676307
5	685.2	79.9	721	12	BG696865
6	500.8	58.4	508	9	AT91495

C	7	500	58.3	508	9	AT732539	AT732539 n101f09.x
C	8	499.2	58.2	508	9	AT913125	AT913125 a656g09.y
C	9	450	52.4	488	9	AA709667	AA709667 z196f02.s
C	10	383	44.6	483	10	AM082062	AM082062 xb59g06.x
C	11	350.8	40.9	913	12	BG676779	BG676779 602623367
C	12	334.6	39.0	341	9	AT9191964	AT9191964 nn90g08.y
C	13	325.4	37.9	374	9	AA505923	AA505923 n101f09.s
C	14	315	36.7	323	9	AT732667	AT732667 nn90g08.x
C	15	293.2	34.2	322	9	AT909857	AT909857 QV-BT225-
C	16	288.2	32.6	325	9	AT909862	AT909862 QV-BT225-
C	17	275.8	32.1	323	9	AA601601	AA601601 nn90g08.s
C	18	272.6	31.8	840	12	BG681217	BG681217 602629361
C	19	243	28.3	321	10	AAW057561	AAW057561 wy60g06.x
C	20	237.8	27.7	537	10	BE012482	BE012482 121944 MA
C	21	229	26.7	444	10	AA6464722	AA6464722 BP230016B
C	22	215.2	25.1	240	9	AT909853	AT909853 QV-BT225-
C	23	214	24.9	510	10	AAW787098	AAW787098 120812 MA
C	24	211.2	24.6	823	12	BG676223	BG676223 602622621
C	25	211.2	24.6	830	12	BG695851	BG695851 602657814
C	26	211.2	24.6	850	12	BG674179	BG674179 602619819
C	27	210.4	24.5	603	12	BG740422	BG740422 602633810
C	28	209.4	24.4	589	12	BG697978	BG697978 602659118
C	29	208.4	24.3	621	12	BG743500	BG743500 602635530
C	30	198.4	23.1	612	12	BG742955	BG742955 602632055
C	31	187.8	21.9	593	10	BE583734	BE583734 4-4B-HA P
C	32	183.6	21.4	585	10	BE583164	BE583164 1-12F-WY
C	33	183.4	21.4	897	12	BG698929	BG698929 602703348
C	34	182.8	21.3	546	10	AAV06393	AAV06393 AV606393
C	35	182.2	21.2	599	14	BQ245980	BQ245980 TA615017F
C	36	181.8	21.2	577	14	BQ294870	BQ294870 WHE2855_D
C	37	180.6	21.0	574	12	BF259672	BF259672 HVSMEF001
C	38	180.6	21.0	917	11	AK009664	AK009664 Mus muscu
C	39	180.2	21.0	646	14	BQ755173	BQ755173 EBE02-SQ
C	40	180	21.0	539	14	BQ606636	BQ606636 H104K03u
C	41	180	21.0	575	12	BF258676	BF258676 HVSMEF001
C	42	180	21.0	638	10	AAV915211	AAV915211 AV915211
C	43	180	21.0	677	10	AAV921849	AAV921849 AV921849
C	44	180	21.0	700	9	AL506588	AL506588 AL506588
C	45	180	21.0	810	12	BF254128	BF254128 HVSMEF000

ALIGNMENTS

RESULT 1
LOCUS BG697492 867 bp mRNA linear EST 07-MAY-2001
DEFINITION 602660685F1 NCI_CGAP_Skn3 Homo sapiens cDNA clone IMAGE:4803932 5',
mRNA sequence.
ACCESSION BG697492
VERSION BG697492.1 GI:13963770
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 867)
TITLE NIH-MGC http://mgc.nci.nih.gov/.
JOURNAL Unpublished (1999)
CONTACT: Robert Strausberg, Ph.D.
COMMENT Email: cgapbs-remail.nih.gov
Tissue Procurement: James Cleaver, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA
Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC Clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLM10700 row: 1 column: 21
High quality sequence stop: 828.
Location/Qualifiers
1. 867

FEATURES
Source

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4803932"
/lab_host="NCI CGAP Skn4"
/Note="Organ: skin; Vector: pcMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.5kb. Library constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
BASE COUNT      187 a      252 c      296 g      132 t
ORIGIN

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Query Match      88.7%; Score 761.4; DB 12; Length 867;
Best Local Similarity 97.7%; Pred. No. 2.2e-136;
Matches 804; Conservative 0; Mismatches 16; Indels 3; Gaps 3;

Cy 37 CACGAGCTCTGAGACACAGGTTGAGCGCGGTGGGAGCAGCTCGGAGGCTCCGCGAG 96
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Db 1 CACGAGCTCTGAGACACAGGTTGAGCGCGGTGGGAGCAGCTCGGAGGCTCCGCGAG 60

Qy 97 GTGACGAGACGACGAGCATGCGCGGTGAGCTGACTCTGAGAGAGAGGCCAGTACAAA 156
    |||||||
Db 61 GTGACGAGACGACGAGCATGCGCGGTGAGCTGACTCTGAGAGAGAGGCCAGTACAAA 120

Qy 157 AGGCTTCTCCGCGGTGACACGAGTGAAGACGACATCATGCTCCAGAGAGCTGGGCG 216
    |||||||
Db 121 AGGCTTCTCCGCGGTGACACGAGTGAAGACGACATCATGCTCCAGAGAGCTGGGCG 180

Qy 217 CGGCGCTGAAGGCCACGCGCAAGAACCTCTGAGAGGCCAGCTGAAGAACTCATCTCG 276
    |||||||
Db 181 CGGCGCTGAAGGCCACGCGCAAGAACCTCTGAGAGGCCAGCTGAAGAACTCATCTCG 240

Qy 277 AGGTTGACAGCAGCGGCGCAAGTCAAGTTCCAGAGTCTCTGACGCGCGCAAGGA 336
    |||||||
Db 241 AGGTTGACAGCAGCGGCGCAAGTCAAGTTCCAGAGTCTCTGACGCGCGCAAGGA 300

Qy 337 AGGCGAGGCGCGGCTGAGAGACCTGAGAGTCCGCTCCGCGGCTTCGACAGAGTGGCG 396
    |||||||
Db 301 AGGCGAGGCGCGGCTGAGAGACCTGAGAGTCCGCTCCGCGGCTTCGACAGAGTGGCG 360

Qy 397 ACGGCCATCATACCGTGAAGACGCTCAAGCGGCGCCATGCGGCGCTGGGCGAGCGCTGC 456
    |||||||
Db 361 ACGGCCATCATACCGTGAAGACGCTCAAGCGGCGCCATGCGGCGCTGGGCGAGCGCTGC 420

Qy 457 CGCAGAGAGAGCTGACCCCATGATCCGCGAGGCGGAGCTGAGACAGGAGCGGCGTGA 516
    |||||||
Db 421 CGCAGAGAGAGCTGACCCCATGATCCGCGAGGCGGAGCTGAGACAGGAGCGGCGTGA 480

Qy 517 ACTAGAGAGAGTGGCGAGAGTGGTCCGCGAGAGTGAAGCTCCCGGCGCTGTATCCGCT 576
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Db 481 ACTAGAGAGAGTGGCGAGAGTGGTCCGCGAGAGTGAAGCTCCCGGCGCTGTATCCGCT 540

Qy 577 GGCCTGCGCTGAGAGCTTCAAGGCGCACCGCGGCTGCTGCTTTTGTGCGGAGCTCTCG 636
    |||||||
Db 541 GGCCTGCGCTGAGAGCTTCAAGGCGCACCGCGGCTGCTGCTTTTGTGCGGAGCTCTCG 600

Qy 637 GCGAAACCTGCTGCTGAGTGGGAACTGCTCCCGCTGGGAGAGAGGCTTTGCGCTCG 696
    |||||||
Db 601 GCGAAACCTGCTGCTGAGTGGGAACTGCTCCCGCTGGGAGAGAGGCTTTGCGCTCG 660

Qy 697 GGGGCTGGA-TGGGCGCGGCTCGGCGCGCTGGGAGCGGCTCTGCTTGAAGCTTGG 755
    |||||||
Db 661 GGGGCTGGA-TGGGCGCGGCTCGGCGCGCTGGGAGCGGCTCTGCTTGAAGCTTGG 720

Qy 756 GCAGAGAGAGGCTCTTGGGCTGCTGTCGCCCTTGGCCCTCAGTGAAGAGGCGGCT 815
    |||||||
Db 721 GCAGAGAGAGG-CTCTCTGGGCGCTGCGTCCCGCTTGGCTCAGTGAAGAGG-CCCT 778

Qy 816 TAACCCGCAATGATCTAAATAAAGAGCTGCCAGTTCCAAA 858
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Db 779 TCAGCCCGCAATGATCTAAATAAAGAGATTCGAGTTCCAAA 821

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RESULT 2
Bg680086      819 bp      mRNA      linear      EST 01-MAY-2001
LOCUS         602628238p1 NCI_CGAP_Skn4 Homo sapiens cDNA clone IMAGE:4753280 5',
DEFINITION    mRNA sequence.
ACCESSION     Bg680086
VERSION       Bg680086.1 GI:13911483
KEYWORDS      EST.
SOURCE        human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE     1 (bases 1 to 819)
AUTHORS      NIH-MGC http://mgc.nci.nih.gov/.
TITLE        National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL       Unpublished (1999)
COMMENT       Contact: Robert Strausberg, Ph.D.
              Email: cgapbs-remail.nih.gov
              Tissue Procurement: James Cleaver, M.D.
              cDNA Library Preparation: Life Technologies, Inc.
              cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
              DNA sequencing by: Incyte Genomics, Inc.
              Clone distribution: MGC clone distribution information can be
              found through the I.M.A.G.E. Consortium/LLNL at:
              http://image.llnl.gov
              Plate: LHAM10612 row: k column: 09
              High quality sequence stop: 819.
              Location/Qualifiers
                1. 819

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FEATURES

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source
  1. 819
    /organism="Homo sapiens"
    /db_xref="taxon:9606"
    /clone="IMAGE:4753280"
    /clone_id="NCI_CGAP_Skn4"
    /tissue_type="squamous cell carcinoma"
    /lab_host="DH10B (T1 phage-resistant)"
    /Note="Organ: skin; Vector: pcMV-SPORT6; Site_1: NotI;
    Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
    Average insert size 1.5kb. Library constructed by Life
    Technologies. Note: this is a NCI_CGAP Library."

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BASE COUNT      139 a      256 c      300 g      124 t
ORIGIN
Query Match      87.5%; Score 750.8; DB 12; Length 819;
Best Local Similarity 96.6%; Pred. No. 2.4e-134;
Matches 799; Conservative 0; Mismatches 7; Indels 4; Gaps 4;

Qy 4 TCCCGATCCCTGCGCGCTGCTGACACGAGCTCTGAGACAGAGTTGAG 63
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Db 7 TCCCGGATCCTGCGCGCTGCTGACACGAGCTCTGAGACAGAGTTGAG 66

Qy 64 GGCCTGCGGAGCAGCTCGGAGGCTCCGAGGTGACGAGACGAGCATGGCGGTG 123
    |||||
Db 67 GGCCTGCGGAGCAGCTCGGAGGCTCCGAGGTGACGAGACGAGCATGGCGGTG 126

Qy 124 AGCTGACTCTGAGAGAGAGGCCAGTCAAAAAGGCTTTTCCGCGGTTGACACGATG 183
    |||||||
Db 127 AGCTGACTCTGAGAGAGAGGCCAGTCAAAAAGGCTTTTCCGCGGTTGACACGATG 186

Qy 184 GAAACGACATCAATCCAGAGAGCTGGGCGCGGCTGTAAGGCCACGGCAAGAAC 243
    |||||||
Db 187 GAAACGACATCAATCCAGAGAGCTGGGCGCGGCTGTAAGGCCACGGCAAGAAC 246

Qy 244 TCTCGAGAGCCAGCTAAGAACTCATCTCCAGGTTGACAGCGAGCGGCGAA 303
    |||||||
Db 247 TCTCGAGAGCCAGCTAAGAACTCATCTCCAGGTTGACAGCGAGCGGCGAA 306

Qy 304 TCAGCTTCAGAGAGTTCTGACGCGGCGCAAGAGGCCAGGCGGCTGAGAGACTGCG 363
    |||||||
Db 307 TCAGCTTCAGAGAGTTCTGACGCGGCGCAAGAGGCCAGGCGGCTGAGAGACTGCG 366

Qy 364 AGGTGCGCTTCCGCGGCTTTCAGACAGATGGGAGCGGCACATCAGCTGAGAGCTCA 423
    |||||||
Db 367 AGGTGCGCTTCCGCGGCTTTCAGACAGATGGGAGCGGCACATCAGCTGAGAGCTCA 426

```


Oy 424 GCGGGCCATGGCGGGCTGGGGCAGCCGCTGCCAGAGAGCGTGGACGCCATGATCC 483
 Db 427 GCGGGCCATGGCGGGCTGGGGCAGCCGCTGCCAGAGAGCGTGGACGCCATGATCC 486
 Oy 484 GCGAGCGCGACGTGAGCAGCAGAGCGGGGTGTAACCTACAGAGAGTTCGGCAGAGTCTCG 543
 Db 487 GCGAGCGCGACGTGAGCAGCAGAGCGGGGTGTAACCTACAGAGAGTTCGGCAGAGTCTCG 546
 Oy 544 CCCAGAGAGTGAAGCTCCCGCTGTGTCCCTGGCTGCGCTGTGAGCTTGAAGGCCAC 603
 Db 547 CCCAGAGAGTGAAGCTCCCGCTGTGTCCCTGGCTGCGCTGTGAGCTTGAAGGCCAC 606
 Oy 604 GCGCCGCTGCTCTTTTGTGCTGGAGCTCCGGGAAACCTGATGGGTGGATGGGAAAC 663
 Db 607 CG-CCGCTGCTCTTTTGTGCTGGAGCTCCGGGAAACCTGATGGGTGGATGGGAAAC 665
 Oy 664 TGCCCTCCCTGGAGAGAGCTTTCGCTCCGGGCGCTGATGGGCGCCCTCGGGCCG 723
 Db 666 TGCCCTCCCTGGAGAGAGCTTTCGCTCCGGGCGCTGATGGGCGCCCTCGGGCCG 725
 Oy 724 CCGGAGAGCCCTCTCTGCTCTGACACCTTGGGAGAGAGAGCTTCTGGGCGCTGCTG 783
 Db 726 -CTGGAGAGCCCTCTCTG-CTCCAGACCTTGGGAGAGAGAGAGCTTCTGGGCGCTGCTG 783
 Oy 784 CCCCTTTGCCCTGACAGTGAATGAGGGCC 813
 Db 784 CCCCTTTG-CTGGCAGTGAATGAGGGCC 812

RESULT 3
 LOCUS Bg743203 830 bp mRNA linear EST 15-MAY-2001
 DEFINITION 602634365P1.NCI_CGAP_Skn3 Homo sapiens cDNA clone IMAGE:4779184 5',
 mRNA sequence.
 ACCESSION Bg743203
 VERSION Bg743203.1 GI:14053856
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 830)
 AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Stransberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: James Cleaver, M.D.
 cDNA Library Preparation: Life Technologies, Inc.
 Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLML10636 row: b column: 17
 High quality sequence stop: 823.
 Location/Qualifiers
 1. 830
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:4779184"
 /clone_lib="NCI_CGAP_Skn3"
 /lab_host="DH10B (Tl phage-resistant)"
 /note="Organ: skin; Vector: pCMV-SPOK6; Site_1: NotI;
 Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
 Average insert size 1.5kb. Library constructed by Life
 Technologies. Note: this is a NCI_CGAP Library."

BASE COUNT 139 a 257 c 303 g 131 t
 ORIGIN
 Query Match 85.9%; Score 737.2; DB 12; Length 830;
 Best Local Similarity 97.3%; Pred. No. 9,6e-132;

Matches 792; Conservative 0; Mismatches 18; Indels 4; Gaps 4;
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 Db 10 TTCCCGGATCCCTGGGCGCTGCTGACCTTGGACCAAGAGCTTGTAGAGCAGAGTTGA 69
 Oy 63 GGGCGGTGGGAGAGAGTCCGAGAGCTCCGAGAGTGCAGAGAGCAGAGCATGAGCGGT 122
 Db 70 GGGCGGTGGGAGAGAGTCCGAGAGCTCCGAGAGTGCAGAGAGCAGAGCATGAGCGGT 129
 Oy 123 GAGTGTACTCTGAGAGAGAGGCCAGTACAAAAGAGCTTTCGCGGTTGACAGCGAT 182
 Db 130 GAGTGTACTCTGAGAGAGAGGCCAGTACAAAAGAGCTTTCGCGGTTGACAGCGAT 189
 Oy 183 GGAAGCGACCAT 241
 Db 190 GGAAGCGACCAT 249
 Oy 242 CCTTCGAGAGGCCAGAGTAAAGAACTATCTCCGAGTTCAGAGAGAGAGAGAGCGA 301
 Db 250 CCTTCGAGAGGCCAGAGTAAAGAACTATCTCCGAGTTCAGAGAGAGAGAGAGCGA 309
 Oy 302 AATCAGCTTCCAGAGATCTGACGCGGCAAGAAAGCCAGAGCGCGCTGAGAGACT 361
 Db 310 AATCAGCTTCCAGAGATCTGACGCGGCAAGAAAGCCAGAGCGCGCTGAGAGACT 369
 Oy 362 GCGAGTGGCTTCCGCGCTTGCAGAGATGGCGAGCGGCAATCAGCTGAGAGAGCT 421
 Db 370 GCGAGTGGCTTCCGCGCTTGCAGAGATGGCGAGCGGCAATCAGCTGAGAGAGCT 429
 Oy 422 CAGCGGGCCATGGCGGCTGGGAGAGCGCTGCGGAGAGAGAGTGGAGCCATGAT 481
 Db 430 CAGCGGGCCATGGCGGCTGGGAGAGCGCTGCGGAGAGAGAGTGGAGCCATGAT 489
 Oy 482 CCGCGAGCGCGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGTTCGAGAGTGT 541
 Db 490 CCGCGAGCGCGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGTTCGAGAGTGT 549
 Oy 542 GCGCCAGAGTGAAGGCTCCGCGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 601
 Db 550 GCGCCAGAGTGAAGGCTCCGCGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 608
 Oy 602 ACCGCGCGCTGCTGCTTGTGCTGAGACTTCGCGGAGAACTGCTGCTGCTGCTGCTG 661
 Db 609 ACCGCGCGCTGCTGCTTGTGCTGAGACTTCGCGGAGAACTGCTGCTGCTGCTGCTG 668
 Oy 662 ACTGCTCTCCCTG-TCGAGAGAGAGCTTTCGCTCCGAGGCTTCGAGAGAGAGCT 720
 Db 669 ACTGCTCTCCCTG-TCGAGAGAGAGCTTTCGCTCCGAGGCTTCGAGAGAGAGCT 728
 Oy 721 CCGCGTGGAGAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 779
 Db 729 CCGCGTGGAGAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 788
 Oy 780 GGTCCCTCTTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 813
 Db 789 GGTCCCTCTTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 822
 RESULT 4
 LOCUS Bg676307 976 bp mRNA linear EST 01-MAY-2001
 DEFINITION 602622717P1.NCI_CGAP_Skn4 Homo sapiens cDNA clone IMAGE:4747661 5',
 mRNA sequence.
 ACCESSION Bg676307
 VERSION Bg676307.1 GI:13907703
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 976)
 AUTHORS NIH-MGC http://mgi.nci.nih.gov/.

Query Match	58.2%	Score 499.2	DB 9	Length 508
Best Local Similarity	99.2%	Pred. No. 4.1e-86		
Matches 501	Conservative 0	Mismatches 4	Indels 0	Gaps 0
OY	3	TTCCCGGATCCCTGGCGGCTGCCTGCATCTGTGACACAGCTCTGAGACAGCAGTGTGA	62	
Db	4	TGCCCGGATTCCTGGGGCTGCCTGCATCTGTGACACAGCTCTGAGACAGCAGTGTGA	63	
OY	63	GGGCGCGTGGGACAGCAGCTCGAGGCTCCGCGAGGTGACAGACAGCAGCAGTGGCCGT	122	
Db	64	GGGCGCGTGGGACAGCAGCTCGAGGCTCCGCGAGGTGACAGACAGCAGCAGTGGCCGT	123	
OY	123	GAGCTGACTCCGAGAGAGAGGCGCAGTACAAAAGGCTTTCTCCGCGGTGACAGGAT	182	
Db	124	GAGCTGACTCCGAGAGAGAGGCGCAGTACAAAAGGCTTTCTCCGCGGTGACAGGAT	183	
OY	183	GGAAACGGCACCATCAATGATCCAGAGAGTGGGCGCGCGCTGMAAGCCACGGCAAGAC	242	
Db	184	GGAAACGGCACCATCAATGATCCAGAGAGTGGGCGCGCGCTGMAAGCCACGGCAAGAC	243	
OY	243	CTCTCGAGAGGCCACGCTAAGAACTCATCTCCGAGTTGACAGCGCAGCGCGGCA	302	
Db	244	CTCTCGAGAGGCCACGCTAAGAACTCATCTCCGAGTTGACAGCGCAGCGCGGCA	303	
OY	303	ATACACTTCCAGAGATTCCTGACGGCGCGCAAGAGAGCCAGGCGCGCTGAGAGACTG	362	
Db	304	ATACACTTCCAGAGATTCCTGACGGCGCGCAAGAGAGCCAGGCGCGCTGAGAGACTG	363	
OY	363	CAGTCCGCTTCCGCGCTTGCAGCAGAGATGAGCAGGCGCACATCAGCTGGAGCAGCTC	422	
Db	364	CAGTCCGCTTCCGCGCTTGCAGCAGAGATGAGCAGGCGCACATCAGCTGGAGCAGCTC	423	
OY	423	AGCGCGCCATGCGGGGCTGGGGCAGCCGCTGCCGAGAGAGACTGAGCCCATGATC	482	
Db	424	AGCGCGCCATGCGGGGCTGGGGCAGCCGCTGCCGAGAGAGACTGAGCCCATGATC	483	
OY	483	CGCGAGCGCCGAGCTGGACAGCAGC	507	
Db	484	CGCGAGCGCCGAGCTGGACAGCAGC	508	

RESULT 9
AA709067/c 488 bp mRNA linear EST 24-DEC-1997
LOCUS 216f02.s1 Soares_fetal_heart.NbH115w Homo sapiens cDNA clone
DEFINITION IMAGE.384795 3' similar to SW:CALM_CHLRE P04352 CALMODULIN. ;, mRNA
sequence.
ACCESSION AA709067.1 GI:2718985
VERSION EST.
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 488)
AUTHORS Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
Krizman,D., Kucaba,T., Lacey,M., Le,N., Lennon,G., Marra,M., Martin,
J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theisling,B.,
White,Y., Wylie,T., Waterston,R. and Wilson,R.
WashU-NCI human EST project
Unpublished (1997)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Possible reversed clone: similarity on wrong strand
Seq primer: -40m13 fwd. RT from Amersham
High quality sequence stop: 321.
Location/Qualifiers

SOURCE		1. .488	/organism="Homo sapiens"
		/db_xref="GDB:1293053"	
		/db_xref="taxon:9606"	
		/clone="IMAGE:384795"	
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		/sex="unknown"	
		/dev_stage="19 weeks"	
		/lab_host="DH10B (ampicillin resistant)"	
		/note="Organ: heart; Vector: pT7SD (Pharmacia) with a modified polylinker; Site.1: Not I; Site.2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAATCTGAAGTGAGGGCGGCCGCACATTCTTTTTTTTTTTT 3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7S vector (Pharmacia). Library was through one round of normalization to a Cot = 5. Library constructed by M.Patima Donaldso. This library was constructed from the same fetus as the fetal lung library, Soares fetal lung NBn19w."	
BASE COUNT	85 a	166 c	162 g 75 t
ORIGIN			
Query Match	52.4%; Score 450;	DB 9;	Length 488;
Best Local Similarity	97.6%; Pred. No.11e-76;		
Matches 478;	Conservative 0;	Mismatches 10;	Indels 2;
Gaps 2;			
OY	369	GCCTTCGCGCCGCTTGACCAGGATGGCAGCGCCACATCACCGTGGACGAGCTCAGCGG	428
Db	488	GCTTTCCGCGCTTGACCAGGATGGCAGCGCCACATCACCGTGGACGAGCTCAGCGG	429
OY	429	GCCATGGCGGGGCTTGGGCGACGCCGTGCCGCGAGAGAGACTGACGCCATCATCCGCGAG	488
Db	428	GCCATGGCGGGGCTTGGGCGACGCCGTGCCGCGAGAGAGACTGACGCCATCATCCGCGAG	369
OY	489	GCCGACGTGGACAGCAGCGCGGGGTGAATACAGAGAGTTGCGCAGAGATGTCGCCAG	548
Db	368	GCCGACGTGGACAGCAGCGCGGGGTGAATACAGAGAGTTGCGCAGAGATGTCGCCAG	309
OY	549	GAGTAGGCTCCCGCTGTGTGCCCGGCGGCTGTGAGGCTTCAAGGGCGACCGCC	608
Db	308	GAGTA-GCTCCCCCGCTGTGTGCCCGGCGGCTGTGAGGCTTCAAGGGCGACCGCC	250
OY	609	GCTGTGCTTTTGTCTGGAGCTCCGCGGAAACCTGTGTGATGGAGAATGCTCT	668
Db	249	GCTGTGCTTTTGTCTGGAGCTCCGCGGAAACCTGTGTGATGGAGAATGCTCT	190
OY	669	CCCCCTGGAGAGAGGCTTGTGGCTCGGCGGCTTGATGCGGCGCCCTGCG	728
Db	189	CCCCCTGGAGAGAGGCTTGTGGCTCGGCGGCTTGATG-CGCGCTCGGCGCCCTGCG	131
OY	729	GAGCCCCTCTGCTTGACACTTGGGCAGAAAGAGGCTCTTGGGCTGTGCTCCCT	788
Db	130	GAGCCCCTCTGCTTGACACTTGGGCAGAAAGAGGCTCTTGGGCTGTGCTCCCT	71
OY	789	TTCGCTCAGTGAATGAGGGCCCTTAACCCGCATTTGATCTAATAAAGAGATGCG	848
Db	70	TTCGCTCAGTGAATGAGGGCCCTTAACCCGCATTTGATCTAATAAAGAGATGCG	11
OY	849	AGTTCCAAA 858	
- Db	10	AGTTCCAAA 1	
RESULT 10			
AM082062/c			
LOCUS	AM082062	483 bp	mRNA linear EST 14-OCT-1999
DEFINITION	xbs9g06.x1 NCI CGAP Esq2 Homo sapiens cDNA clone IMAGE:2580634 3'		
ACCESSION	AM082062		
VERSION	AM082062.1	GI:6037214	
KEYWORDS	EST.		


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/clone="IMAGE:966761"
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/sex="female, pooled"
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/notes="vector: pT73D-Pac (Pharmacia) with a modified
polylinker; 1st strand cDNA was prepared from pooled bulk
breast tumor tissue, and was then primed with a Not I -
oligo(dT) primer. Double-stranded cDNA was ligated to Eco
RI adaptors (Pharmacia), digested with Not I and cloned
into the Not I and Eco RI sites of the modified pT73
vector. This library is the normalized version of
NCI_CGAP_Br1.1. Library was constructed by Bento Soares
and M. Fatima Bonaldo. 61 t

BASE COUNT      68 a      124 c      121 g
ORIGIN

Query Match      37.9%; Score 325.4; DB 9; Length 374;
Best Local Similarity 95.2%; Pred. No. 8.5e-53;
Matches 357; Conservative 0; Mismatches 16; Indels 2; Gaps 2;

QY 483 CGGAGGCGCAGCTGACGACGAGGCGGCTGAACTACGAGAGTTCGCGAGATGCTC 542
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 374 CGGAGGCGCAGCTGACGACGAGGCGGCTGAACTACGAGAGTTCGCGAGATGCTC 315
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 543 GCGGAGAGTGAAGCTCCCGCTGTCTCCCGCTGCGCTCTGAGCTTCAGGGCCA 602
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 314 GCGGAGAGTGAAGCTCCCGCTGTCTCCCGCTGCGCTCTGAGCTTCAGGGCCA 255
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 603 CCGGCGCGCTGCTGTTTGTGCTGAGACTCCGCGGGAACCTGCTGGTGGATGGGAAA 662
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 254 CCGGCGCGCTGCTGTTTGTGCTGAGACTCCGCGGGAACCTGCTGGTGGATGGGAAA 195
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 663 CT-GCTCTCCCGCTGAGAGAGGCTTTCGCTCCGCGGCTGAGTGGCGGCTCCGCGC 721
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 194 CTAGACTCCCGCTGAGAGAGGCTTTCGCTCCGCGGCTGAGTGGCGGCTCCGCGC 136
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 722 CGCTGAGAGCTCTCTCTGCTTCAGACTTGGGCGAGAGAGGCTTCCTGGGCTGG 781
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 135 CGCTGAGAGCTCTCTCTGCTTCAGACTTGGGCGAGAGAGGCTTCCTGGGCTGG 76
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QY 782 TCCCGCTTCCCGCTGAGTGAATGAGGCGGCTTAACCCCGCATTTGATCTAATAAAG 841
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DB 75 TCCCGCTTCCCGCTGAGTGAATGAGGCGGCTTAACCCCGCATTTGATCTAATAAAG 16
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QY 842 ACTGCGAGATTCCA 856
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DB 15 ACTGCGAGATTCCA 1
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RESULT 14      323 bp      mRNA      linear      EST 13-DEC-1999
AI732667/c      n90908.x5 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1098494 3'
LOCUS
DEFINITION
ACCESSION      AI732667
VERSION
KEYWORDS
SOURCE
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
1 (bases 1 to 323)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cga@bbs.fda.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmett-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.

```

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DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LNLN at:
www.bio.lnln.gov/bdrp/image/image.html

This read is a RESSEQUENCE of a previously sequenced human clone
Original clone citation: National Cancer Institute, Cancer Genome
Anatomy Project (CGAP), Tumor Gene Index
This read has been verified (found to hit its original self in the
correct orientation)
Insert length: 418 Std Error: 0.00
Seq primer: -400P from G1bco.
Location/Qualifiers
1. 323
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/clone_lib="NCI_CGAP_Br2"
/sex="female, pooled"
/tissue_type="breast"
/lab_host="DH10B"
/notes="vector: pT73D-Pac (Pharmacia) with a modified
polylinker; 1st strand cDNA was prepared from pooled bulk
breast tumor tissue, and was then primed with a Not I -
oligo(dT) primer. Double-stranded cDNA was ligated to Eco
RI adaptors (Pharmacia), digested with Not I and cloned
into the Not I and Eco RI sites of the modified pT73
vector. This library is the normalized version of
NCI_CGAP_Br1.1. Library was constructed by Bento Soares
and M. Fatima Bonaldo. 45 t

BASE COUNT      64 a      103 c      111 g
ORIGIN

Query Match      36.7%; Score 315; DB 9; Length 323;
Best Local Similarity 98.5%; Pred. No. 8.4e-51;
Matches 318; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 323 GAGATGCTGCGCCAGAGAGGCTCCCGCTGTGCTCCCGCTGCGCTTGAGCC 264
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 593 TTGAGGCGCACCGCGCTGCTGCTTGTGCTGAGACTCCGCGGGAACCTGTCGGT 652
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 263 TTGAGGCGCACCGCGCTGCTGCTTGTGCTGAGACTCCGCGGGAACCTGTCGGT 204
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 653 GGATGGAAACTGCTCCCGCTGAGAGAGGCTTTCGCTCCGCGGCTGAGTGGCG 712
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 203 GGATGGAAACTGCTCCCGCTGAGAGAGGCTTTCGCTCCGCGGCTGAGTGGCG 144
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 713 CCTGCGGCGCGCTGCGAGCCCTCTGCTTGAACCTTGGGCAAGAGGCTCTCT 772
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 143 CCTGCGGCGCGCTGCGAGCCCTCTGCTTGAACCTTGGGCAAGAGGCTCTCT 84
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 773 TGGGCGCTGTCCTCCCTTGGCGCTGAGTGAAGGCGGCTTAACCCCGCATTTGAT 832
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 83 TGGGCGCTGTCCTCCCTTGGCGCTGAGTGAAGGCGGCTTAACCCCGCATTTGAT 24
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 833 AAATGAAGACTGCGAGTTCCA 855
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RESULT 15      322 bp      mRNA      linear      EST 30-MAR-2000
AI909857/c      n909857 050599-063 BR225 Homo sapiens cDNA, mRNA sequence.
LOCUS
DEFINITION
ACCESSION      AI909857
VERSION
KEYWORDS
SOURCE
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

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REFERENCE
AUTHORS

1 (bases 1 to 322)
 Dias Neto, E., Garcia Correa, R., Verjowski-Almeida, S., Briones, M.R.,
 Nagai, M.A., de Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
 Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H.,
 Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare
 M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
 Simpson, A.J.

TITLE

Shotgun sequencing of the human transcriptome with ORF expressed
 sequence tags

JOURNAL
MEDLINE

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 20202663

COMMENT

Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome
 Project. This entry can be seen in the following URL
 (<http://www.ludwig.org.br/seq/gethtml.pl?tl=QVet2-QV-BT225-063.html>
 6t3-0505986t4-1)
 Seq primer: puc 18 forward.
 Location/Qualifiers

FEATURES

source

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 /db_xref="taxon:9606"
 /clone_lib="BT225"
 /sex="female"
 /dev_stage="Adult"
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 Smat; A mini-library was made by cloning products derived
 from ORESTES PCR (U.S. Letters Patent application No. 196
 716 - Ludwig Institute for Cancer Research) profiles
 into the pUC 18 vector. Reverse transcription of tissue
 mRNA and cDNA amplification were performed under low
 stringency conditions."

BASE COUNT 64 a 106 c 107 g 45 t
 ORIGIN

Query Match

Best Local Similarity 94.4%; Score 293.2; DB 9; Length 322;

Matches 304; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

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Db 322 CCAAGCTGACACGAGCGGGGCTTACCTACGAGAGTTCGCGAGATGCTGCCACGA 263
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OY 550 AGTGAGGCTCCCGCGCTGTGTCTCCCTGGCTGGCTCTGAGCCTCAGGGCCACGCCCG 609
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OY 610 CTGCTGCTTTTGTGCTGGGACTCTCCGGGGAACCTGTGTGGATGGGAACCTGCTC 669
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Db 202 TTGCTGCTTTTGTGCTGGGACTCTCCGGGGAACCTGTGTGGATGGGAACCTGCTC 143
    ||||||| ||||||||| || ||||||| ||||||||| |||||||||
OY 670 CCCCTGGAGGAAGCTTGGCGCTCCGGGGCTGGATGGGGCGCCCTCGGGCGCGCTGCG 729
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Db 142 CCCCTGGAGGAAGCTTGGCGCTCCGGGGCTGGATGGGGCGCCCTCGGGCGCGCTGCG 83
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OY 730 AGCCCTCTCTGCTTCAAGACTTGGGCAAGAGAGCCCTCTTGGGCGCTGCTCCCTT 789
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Db 82 AGCCCTCTCTGCTTCAAGACTTGGGCAAGAGAGCCCTCTTGGGCGCTGCTCCCTT 23
    ||||||| ||||||||| || ||||||| ||||||||| |||||||||
OY 790 TGGCTGCACTGATGAGGCG 811
    ||||||| ||||||||| || ||||||| ||||||||| |||||||||
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Search completed: May 16, 2003, 01:11:33
 Job time : 1740 secs

Best Local Similarity 57.6%; Pred. No. 7e-16;
Matches 245; Conservative 0; Mismatches 171; Indels 9; Gaps 1;

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QY 183 GGAAGCGCAGCATCATATGCCAGAGCTGGCGCGCTGAGAGCCACAGGCAAGAAC 242
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 3075 GGAAGTGGAGCATGACGAGCAAGAGCTGAAGTGGCCATGAGACGCTGGCTTCGAA 3134
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QY 243 CTCTGGAGGCCAGCTAAAGAACTCATCTCCGAGCTTGACAGCAGCGGCGAGGAA 302
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DB 3135 CCCAGAGAACGAGATGAGAAAGAAATGATCTCCGAGGTGACAGGAGGACGCGGGAAG 3194
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QY 303 ATCAGCTTCAGGAGTTCCTGACGCGGCGGCAAGAG-----GCCAGGCGCGGCTTG 353
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DB 3255 GAAGAAATCTGTAAGGCTTCAGGCTCTTGATGACGATGAGACCGGGAAGATCTGCTTC 3314
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QY 414 GACGAGCTAGCGGGGCGCATGGCGGGGCTGGGCGACGCCCTGCCGAGAGAGCTGGAC 473
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DB 3315 AAAAAGCTGAGCGCTGTGGCCAAAGCTGGGAGAGACCTCAGGATGAGAGCTGACG 3374
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QY 474 GCGATGATCGGAGGAGCGAGCTGAGCAAGAGCGGGGCTGACAGAGAGAGCTCGCG 533
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RESULT 4 US-08-818-253-1

; Sequence 1, Application US/08818253
; Patent No. 5998204

GENERAL INFORMATION:

APPLICANT: Tsien, Roger Y.
APPLICANT: Miyawaki, Atsushi
TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR
NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FastSeq for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/818,253
FILING DATE: 14-MAR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER:

ATTORNEY/AGENT INFORMATION:
NAME: Hallie, Ph.D., Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07257/043001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
TELEFAX: 619/678-5099
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:

LENGTH: 1929 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 1...1926
US-08-818-253-1

Query Match 14.3%; Score 122.6; DB 2; Length 1929;
Best Local Similarity 56.0%; Pred. No. 9e-16;
Matches 258; Conservative 0; Mismatches 194; Indels 9; Gaps 1;

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QY 105 GAGCGAGGATGGCGCGGTGAGTCTGCTGAGAGAGAGGCCAGTACAAAAGGCTTTC 164
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QY 165 TCCGCGGTGACACGATGGAACGGCACCATCATATGCCAGAGAGCTGGCGCGGCTG 224
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DB 739 TCATTAATTCAGAAAGATGGGAGCGCACCATCACCACAAAGAACTTGGCACGTTATG 798
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QY 225 AAGGCCAGGCGCAAGAACTCTCGAGAGCGCCAGCTAAGAAACTCATCTCCGAGTTGAC 284
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DB 799 AGGTCCCTTGACCAAAACCAACGAGAGCAAGATTCAGAGATATGATCAATGAATCGAT 858
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QY 285 AGCGAGCGGAGCGCAAAATACCTTCAGAGATTCCTGACGCG-----GCCAAG 335
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DB 859 GCTGATGGCAATGAACGATTTACTTCTGAAATTTCTTACTATGATGGCTACAAAATG 918
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QY 336 AAGGCCAGGCGCGCGCTGAGAGCTGACAGTGGCTTCGCGCTTCGACAGAGATGGC 395
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DB 919 AAGGACACAGACAGCAAGAGAAATCCGAGAAAGCATTCGTTTTCGAAAGATGGG 978
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QY 396 GAGCGCACATCACCGTGAAGAGCTCAGCGCGGCGCATGGCGGCGCTGGGCGACCGCTG 455
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DB 1099 AACTATGAAGAGTTGTACAAATGATGACAGCAAAAGGGGG 1139
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RESULT 5 US-08-818-253-5

; Sequence 5, Application US/08818253
; Patent No. 5998204

GENERAL INFORMATION:

APPLICANT: Tsien, Roger Y.
APPLICANT: Miyawaki, Atsushi
TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR
NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FastSeq for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/818,253
FILING DATE: 14-MAR-1997
PRIOR APPLICATION DATA:

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; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Ph.D., Lisa A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 07257/043001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1929 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 1...1926
; US-08-818-253-5

```

```

Query Match      14.3%; Score 122.6; DB 2; Length 1929;
Best Local Similarity 56.0%; Pred. No. 9e-16;
Matches 258; Conservative 0; Mismatches 194; Indels 9; Gaps 1;

```

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QY 105 GAGCAGGATGCGCGGTGAGCTGCTCTGAGAGAGAGCCCACTACAAAAGGCTTTC 164
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 679 GCCCGCCGATGATGACCACTGACAGAAAGAGAGATTCGAGATTCAAAAGAGCCCTTC 738
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 165 TCCCGGTTGACAGGATGAAAGGCGACATCAATGCCAGAGAGTGGGGCGCGCTG 224
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 739 TCATTATTCGACAGATGGGAGCGCACATCACCAAGAAAGACTTGGACCGTTATG 798
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 225 AAGCCAGGCGCAAGAACTCTCGAGGCGCAGCTAAGAAACTATCTCCAGATTGAC 284
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 799 AGTCGCTTGACAAAACCCAGAAAGCAATTCGAGATGATGATCAATGAAGATGAT 858
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 285 AGCAGCGCGGCGGAAATGAGTTCAGAGATTCCTGACAGGGG-----GCAAG 335
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 859 GCTATGCAATGGAACGATTACTTCTGTAATTTCTTACTATGATGGCTAGAAAATG 918
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 336 AAGCCAGGCGCGCGCTGAGAGACCTGCGAGCTGCTCCGCGCTTCGACAGATGAC 395
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 919 AAGGACACAGACAGAGAAAGAAATCCGAGAACATTCCTGTTTGGACAAAGATGG 978
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 396 GACGCGCATACCGCTGAGAGAGCTCAGCGGCGCATGCGGGGCTGCGGAGCCGCTG 455
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 979 AACGCTACATCAGCGCTGCTCAGTACGTACGTACGTACGTAACAACTCGGGAGAGTTA 1038
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 456 CCGCAGAGAGAGCTGAGCGCATGATCGGAGCGCGAGCGAGCCAGAGAGCGGGTG 515
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1039 ACAATGAGAGATTGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTA 1098
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 516 AACTACGAGAGATTGCGGAGAGATCTCGCCAGAGAGTGAGG 556
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1099 AACTATGAGAGTTTGTATCAAAATGATGACACCAAGGGGG 1139
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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RESULT 6
; Sequence 1, Application US/0818252B
; Patent No. 6197928
; GENERAL INFORMATION:
; APPLICANT: Tsien, Roger Y.
; APPLICANT: Miyawaki, Atsushi
; TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR
; TITLE OF INVENTION: DETECTION OF ANALYTES
; FILE REFERENCE: 07257/042001
; CURRENT APPLICATION NUMBER: US/08/818.252B
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1

```

```

; LENGTH: 1929
; TYPE: DNA
; ORGANISM: Aequorea victoria
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (0)...(1926)
; US-08-818-252-1

```

```

Query Match      14.3%; Score 122.6; DB 4; Length 1929;
Best Local Similarity 56.0%; Pred. No. 9e-16;
Matches 258; Conservative 0; Mismatches 194; Indels 9; Gaps 1;

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```

QY 105 GAGCAGGATGCGCGGTGAGCTGCTCTGAGAGAGAGCCCACTACAAAAGGCTTTC 164
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 679 GCCCGCCGATGATGACCACTGACAGAAAGAGAGATTCGAGATTCAAAAGAGCCCTTC 738
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 165 TCCCGGTTGACAGGATGAAAGGCGACATCAATGCCAGAGAGTGGGGCGCGCTG 224
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 739 TCATTATTCGACAGATGGGAGCGCACATCACCAAGAAAGACTTGGACCGTTATG 798
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 225 AAGCCAGGCGCAAGAACTCTCGAGGCGCAGCTAAGAAACTATCTCCAGATTGAC 284
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 799 AGTCGCTTGACAAAACCCAGAAAGCAATTCGAGATGATGATCAATGAAGATGAT 858
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 285 AGCAGCGCGGCGGAAATGAGTTCAGAGATTCCTGACAGGGG-----GCAAG 335
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 859 GCTATGCAATGGAACGATTACTTCTGTAATTTCTTACTATGATGGCTAGAAAATG 918
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 336 AAGCCAGGCGCGCGCTGAGAGACCTGCGAGCTGCTCCGCGCTTCGACAGATGAC 395
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 919 AAGGACACAGACAGAGAAAGAAATCCGAGAACATTCCTGTTTGGACAAAGATGG 978
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 396 GACGCGCATACCGCTGAGAGAGCTCAGCGGCGCATGCGGGGCTGCGGAGCCGCTG 455
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 979 AACGCTACATCAGCGCTGCTGTAATTCAGTACGTACGTACGTAACAACTCGGGAGAGTTA 1038
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 456 CCGCAGAGAGAGCTGAGCGCATGATCGGAGCGCGAGCCAGCTGAGACAGAGCGGGTG 515
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1039 ACAATGAGAGATTGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTA 1098
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 516 AACTACGAGAGATTGCGGAGAGATCTCGCCAGAGAGTGAGG 556
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1099 AACTATGAGAGTTTGTATCAAAATGATGACACCAAGGGGG 1139
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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RESULT 7
; Sequence 5, Application US/0818252B
; Patent No. 6197928
; GENERAL INFORMATION:
; APPLICANT: Tsien, Roger Y.
; APPLICANT: Miyawaki, Atsushi
; TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR
; TITLE OF INVENTION: DETECTION OF ANALYTES
; FILE REFERENCE: 07257/042001
; CURRENT APPLICATION NUMBER: US/08/818.252B
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 1929
; TYPE: DNA
; ORGANISM: Aequorea victoria
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (0)...(1926)
; US-08-818-252-5

```

```

Query Match      14.3%; Score 122.6; DB 4; Length 1929;
Best Local Similarity 56.0%; Pred. No. 9e-16;
Matches 258; Conservative 0; Mismatches 194; Indels 9; Gaps 1;
QY 105 GAGCAGGATGCGCGGTGAGCTGCTCTGAGAGAGAGCCCACTACAAAAGGCTTTC 164

```


QY 165 TCCTGGGTTGACAGCGATGAAAGCGACATCAATGCCAGAGCTGGGGCGGCGCTG 224
 Db 739 TCATTATTCGACAAAGATGGGAGCGCACATACACCAAGAACTTGGCACCGTTATG 798
 QY 225 AAGGCCAGGCGAAGAACTCTCCGAGAGGCCAGCTAAGAAACTATCTCCGAGTTAC 284
 Db 799 AGGTGCTTGGACAAACCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 858
 QY 285 AGCGAGCGAGCGAGCAATCAGCTTCCAGAGTCTGAGCGCG-----GCAAG 335
 Db 859 GCTGATGCAATGGAAGATTTACTTCTGATTTCTTACTATGATGGCTAGAAAAATG 918
 QY 336 AAGCGAGCGCGCGCTGAGAGACCTGAGTCCGCTTCCGCGCTTCCGAGAGAGTGC 395
 Db 919 AAGGACACAGAGAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 978
 QY 396 GACGCGCATATCAGCTGAGAGAGCTCAGGGGGGCGGAGCGGCGAGCGCTG 455
 Db 979 AAGCGCTATCATCAGCGCTGCTGATTTACGTACGTCATGACAAACCTCGGGAGAGTTA 1038
 QY 456 CCGCAGAGAGAGCTGAGCGCATGATCCGAGCGAGCGAGCGAGCGAGCGAGCGT 515
 Db 1039 ACAGATGAAGAAGTTGATGAATGATGAAGGAGAGATATGATGATGATGATGATG 1098
 QY 516 AACTACGAGAGCTTCCGAGAGTCTCGCCAGAGAGTACG 556
 Db 1099 AACTATGAAGAAGTTGATGAATGATGATGATGATGATGATGATGATGATGATG 1139

RESULT 10

US-08-818-253-7
 : Sequence 7, Application US/08818253
 : Patent No. 5998204
 : GENERAL INFORMATION:

APPLICANT: Tsien, Roger Y.
 APPLICANT: Miyawaki, Atsushi
 TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR
 TITLE OF INVENTION: DETECTION OF ANALYTES
 NUMBER OF SEQUENCES: 61
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Fish & Richardson P.C.
 STREET: 4225 Executive Square, Suite 1400
 CITY: La Jolla
 STATE: CA
 COUNTRY: USA
 ZIP: 92037

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: Windows 95
 SOFTWARE: FastSeq for Windows Version 2.0b
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/818,253
 FILING DATE: 14-MAR-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:

FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Hallie, Ph.D., Lisa A.
 REGISTRATION NUMBER: 38,347
 REFERENCE/DOCKET NUMBER: 07257/043001
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 619/678-5070
 TELEFAX: 619/678-5099

INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1971 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 FEATURE:

NAME/KEY: Coding Sequence
 LOCATION: 1...1968
 US-08-818-253-7

Query Match 14.3%; Score 122.6; DB 2; Length 1971;
 Best Local Similarity 56.0%; Pred. No. 9.1e-16;
 Matches 258; Conservative 0; Mismatches 194; Indels 9; Gaps 1;

QY 105 GACGAGCGATGCGCGGAGTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 164
 Db 727 GCGCGCGCGATGATGACCACTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 786
 QY 165 TCCTGGGTTGACAGCGATGAAAGCGACATCAATGCCAGAGCTGGGGCGGCGCTG 224
 Db 787 TCATTATTCGACAAAGATGGGAGCGCACATACCAAGCAAGCAAGCAAGCAAGCA 846
 QY 225 AAGGCCAGGCGAAGAACTCTCGAGAGCGCCAGCTAAGAAACATCTCCGAGTTAC 284
 Db 847 AGGTGCTTGGACAAACCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 906
 QY 285 AGCGAGCGAGCGGCAATCAGCTTCCAGAGAGTCTGAGCGCG-----GCAAG 335
 Db 907 GCTGATGCAATGGAAGATTTACTTCTGATTTCTTACTATGATGGCTAGAAAAATG 966
 QY 336 AAGCGAGCGCGCGCTGAGAGACCTGAGTCCGCTTCCGCGCTTCCGAGAGAGTGC 395
 Db 967 AAGGACACAGAGAGCAAGAGAGAAATCCGAGAGCAATTCCTGTTTGGACAGAGTGG 1026
 QY 396 GACGCGCATATCAGCTGAGAGAGCTCAGGGGGGCGGAGCGGCGAGCGCGCTG 455
 Db 1027 AAGCGCTATCATCAGCGCTGCTGATTTACGTACGTCATGACAAACCTCGGGAGAGTTA 1086
 QY 456 CCGCAGAGAGAGCTGAGCGCATGATCCGAGCGAGCGAGCGAGCGAGCGAGCGT 515
 Db 1087 ACAGATGAAGAAGTTGATGAATGATGAAGGAGAGAGATATGATGATGATGATGATG 1146
 QY 516 AACTACGAGAGCTTCCGAGAGTCTCGCCAGAGAGTACG 556
 Db 1147 AACTATGAAGAAGTTGATGAATGATGATGATGATGATGATGATGATGATGATG 1187

RESULT 11

US-08-818-252-7
 : Sequence 7, Application US/08818252B
 : Patent No. 6197928
 : GENERAL INFORMATION:

APPLICANT: Tsien, Roger Y.
 APPLICANT: Miyawaki, Atsushi
 TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR
 TITLE OF INVENTION: DETECTION OF ANALYTES
 FILE REFERENCE: 07257/042001
 CURRENT APPLICATION NUMBER: US/08/818,252B
 CURRENT FILING DATE: 1997-03-14
 NUMBER OF SEQ ID NOS: 56
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 7

LENGTH: 1971
 TYPE: DNA
 ORGANISM: Aequorea victoria
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (0)...(1968)
 US-08-818-252-7

Query Match 14.3%; Score 122.6; DB 4; Length 1971;
 Best Local Similarity 56.0%; Pred. No. 9.1e-16;
 Matches 258; Conservative 0; Mismatches 194; Indels 9; Gaps 1;

QY 105 GACGAGCGATGCGCGGAGTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 164
 Db 727 GCGCGCGCGATGATGACCACTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 786
 QY 165 TCCTGGGTTGACAGCGATGAAAGCGACATCAATGCCAGAGCTGGGGCGGCGCTG 224


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Db 787 TCATTATTCGACAGAGATGGGAGCGGACACATCACCAAGAAAGTAATGGACCGTTATG 846
QY 225 AAGGCCACGGCCAGAACACTCTTCGAGGCCACCTAGGAAGTAATCTCCAGGTTGAC 284
Db 847 AGGTGCTTGGACAAAACCAACGGAAGAGATTCAGATATGATCAATGAGTCGAT 906
QY 285 AGCGACGGGAGGAGGAAATACGCTTCAGAGATTCCTGACGGCG-----GCAAGG 335
Db 907 GCTGATGGCAATGGAACGATTACTTCTGTAATTTCTTACTATGATGGCTAGAAAAATG 966
QY 336 AAGGCCAGGCGCGGCTGAGACCTGACAGCTCGCCTTCGCGCTTCGACACAGATGCG 395
Db 967 AAGGACACAGACAGCAAGAGAAATCGAAGAACATTCGTTTGTGACAAAGATGGG 1026
QY 396 GACGGCAATACACCTGAGACAGCTCAGCGGGCCATGCGGGGCTGGGGGACCGCTG 455
Db 1027 AACGGCTACATAGCGCTCTCAGTTACGTCAAGTCATGACAAACCTCGGGAGAGTTA 1086
QY 456 CCGCAGAGAGCTGAGCCATGATCCGAGCGGACGAGCGGAGGAGGCGGCTG 515
Db 1087 ACAGATGAAGAGTGTATTAATGATAGGGAAGCAAGATATGATGTCGATGCGCAAGTA 1146
QY 516 AACTACGAGAGTTGCGGAGATCTCGCCAGAGAGTGAAG 556
Db 1147 AACTATGAAGAGTTGTACAAATGATGACAGCAAGAGGGGG 1187

```

RESULT 12
US-08-100-874-1
Sequence 1, Application US/08100874
Patent No. 5498533

```

GENERAL INFORMATION:
APPLICANT: Poovalah, B. W.
APPLICANT: Takezawa, D.
APPLICANT: Han, T. J.
APPLICANT: An, G. H.
TITLE OF INVENTION: Control of Growth and Development of
TITLE OF INVENTION: Potato Plants
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Harness, Dickey & Pierce
STREET: P. O. Box 828
CITY: Bloomfield Hills
STATE: MI
COUNTRY: USA
ZIP: 48303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/100.874
FILING DATE: July 30, 1993
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Smith, Dean F.
REFERENCE/DOCKET NUMBER: 7555-00004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (313) 641-1600
TELEFAX: (313) 641-0270
TELEX: 287637 Harness UR
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 906 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHEICAL: NO
ORIGINAL SOURCE:
ORGANISM: Solanum tuberosum

```

INDIVIDUAL ISOLATE: P-PCM-1
FEATURE:
NAME/KEY: CDS
LOCATION: 81..530
US-08-100-874-1

Query Match 12.9%; Score 110.4; DB 1; Length 906;
Best Local Similarity 54.6%; Pred. No. 26-13;
Matches 247; Conservative 0; Mismatches 196; Indels 9; Gaps 1;

```

QY 114 ATGCGCGTGTAGCTGACTCTGAGAGAGAGCCCACTACAAAAAGCTTTCGCGGTT 173
Db 81 ATGGCAGACAGCTGACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 140
QY 174 GACACGATGGAAGGACGACATCATGCCCCAGAGACTGGCGCGGCTGAAAGCCAG 233
Db 141 GACAAAGATGGCGATGCTGTATTAATACCAAGAGAGAGAGAGAGAGAGAGAGAG 200
QY 234 GGCAGAACCTCTCGGAGGCGCCAGTAAGAAACTCATCTCCAGAGTTGACAGCAGGC 293
Db 201 GGTCAATAATCCCACTGACAGCTGACAGAGATATGATCAGTGAACCTGATGATCAG 260
QY 294 GACGCGAAATCAGCTTCCAGAGTTCTGA-----CGCGGCAAGAAAGCCAGG 344
Db 261 AATGGAACCATGATTTTCCAGAGTTCTGAATCTGATGACAGTAAGATGAAGAGACT 320
QY 345 GCGGCGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 404
Db 321 GATTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 380
QY 405 ATCACCCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 464
Db 381 ATTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 440
QY 465 GAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 524
Db 441 GAGGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 500
QY 525 GAGTTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 556
Db 501 GAGTTGCTCCGATGATGCTTCCCAAGAGTAG 532

```

RESULT 13
US-09-239-909-1
Sequence 1, Application US/09239909
Patent No. 6284952
GENERAL INFORMATION:
APPLICANT: Kumho Petrochemical Co. Ltd.
TITLE OF INVENTION: Transgenic Plants with Divergent SCAM4 or SCAM5 Gene to Achieve
FILE REFERENCE: P99-2-6
CURRENT APPLICATION NUMBER: US/09/239.909
FILING DATE: 1999-01-29
EARLIER APPLICATION NUMBER: EP 99300136.1
EARLIER FILING DATE: 1999-01-08
NUMBER OF SEQ ID NOS: 4
SOFTWARE: KOPATIN 1.0
SEQ ID NO: 1
LENGTH: 1401
TYPE: DNA
ORGANISM: G. max calmodulin4 (SCAM4)
FEATURE:
NAME/KEY: CDS
LOCATION: (657)..(1106)
US-09-239-909-1

Query Match 11.0%; Score 94.8; DB 4; Length 1401;
Best Local Similarity 53.0%; Pred. No. 2-10;
Matches 232; Conservative 0; Mismatches 197; Indels 9; Gaps 1;
QY 113 CATGCGCGGTGAGCTACTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 172
Db 656 CATGCGAGATATCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 715

QY 173 TGACACGATGAAACGGCCACCATTATGCCAGAGCTGGGCGGCGCTGAAGGCCAC 232
Db 716 TGACAAATGAGATGCTGCTACCTAGTGAAGAACTCCATCTGATTCGGTCAAT 775
QY 233 GGGGAGAAACCTCTCGAGGCGCCAGCTAAGAAACTCTCCAGAGTTGACAGGAGG 292
Db 776 GGATCGAAGCCCACTGAGAGAGAGCTCAAGATATGATTAAGAGTGCATGAGATG 835
QY 293 CGAGCGGCAATACAGCTTCAGAGATTCCTGA-----CGGCGGCAAGAAAGCCAG 343
Db 836 CAATGGAACCATTTGATTTGAGAGTTCTTGAGCTTGATGCGCAAGAAAGTTAAAGAC 895
QY 344 GGGCGGCTGAGAGACCTGACAGTCCGCTCCGCGCTTCGACCAAGATGCGAGCGCA 403
Db 896 TGATGACAGAGGAGGAGCTCAAGAAAGCTTCAGGTTTTCACAAAGATCAAAATGCGTA 955
QY 404 CATCACCTGACACGAGCTCAGGCGGCGCATGCGGCGCTGGGCGCAGCGCTGCGCAGCA 463
Db 956 CATATCAGTATGATGATGAGACAGATATGATCAATATAGGGGAAAACTAACCGATGA 1015
QY 464 GAGCTGAGCCCATGATCCCGAGAGCGGAGCTGAGACGAGGCGGCGTGAAGTACGA 523
Db 1016 AGAGTGAAGAGATGATTAAGAAAGCATTTGAGCGGTATGCGCAAGTTAACTATGA 1075
QY 524 GAGCTGCGGAGATGCT 541
Db 1076 GGAATTCGTCAAGATGAT 1093

RESULT 14

US-09-239-909-3
; Sequence 3, Application US/09239909
; Patent No. 6284952
; GENERAL INFORMATION:
; APPLICANT: Kumo Petrochemical Co. Ltd.
; TITLE OF INVENTION: Transgenic Plants with Divergent Scam4 or Scam5 Gene to Achieve
; FILE REFERENCE: p99-2-6
; CURRENT APPLICATION NUMBER: US/09/239, 909
; EARLIER FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: EP 99300136.1
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: KOPATIN 1.0
; SEQ ID NO 3
; LENGTH: 916
; TYPE: DNA
; ORGANISM: G. max calmodulin5 (Scam5)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (69)..(518)
US-09-239-909-3

Query Match 10.3%; Score 88.4; DB 4; Length 916;
Best Local Similarity 52.1%; Pred. No. 3; 7e-09;
Matches 226; Conservative 0; Mismatches 201; Indels 9; Gaps 1;

QY 113 CATGCGCGGTGAGTCTGCTGAGAGAGAGCCAGTACAAAAGGCTTCTCCGCGGT 172
Db 68 CATGGCAGATGTTCTGAGTGAAGAAAGATAGTATGATCAAGAAAGGCTTGGCTTGT 127
QY 173 TGACACGATGAAACGGCCACCATCAATGCCAGAGAGTGGGCGGCGCTGAAGGCCAC 232
Db 128 TGACAAAGATGATGATGCTGATCTAGCTGAGCAATTTGTCACGGTTATCCGGTCAAT 187
QY 233 GGGCAAGAACTCTCGAGGCGCCAGCTAAGAAACTCTCCAGGTTGACAGGAGG 292
Db 188 GGTTCAGAAACCCACAGAAAGAGCTTCAAGACATGATTAACAGAGTATGACATG 247
QY 293 CGAGCGGCAATCACTTCAGAGTTCCTGA-----CGGCGGCAAGAAAGGCCAG 343
Db 248 TAATGAAACCATGATTTGTTGAGTTTTCAGCTTAATGCGCAAGAAATGAAGGAAC 307

QY 344 GGGCGGCTGAGAGACCTGACAGTCCCTCCGCGCTTCGACCAAGATGCGGAGGCCA 403
Db 308 TGATGAAGAGAAATGCTCAAGAGAGGCTTTCAGGTTTTCACAAAGATCAAAATGCGTA 367
QY 404 CATCACCTGAGACGAGCTCAGGCGGCGCATGCGGCGCTGGGCGCAGCGCTGCGCAGCA 463
Db 368 CATTTACCAAGTGAAGTGAACACGTTATGATCAATGTTGGGAAAACTAATGATGA 427
QY 464 GAGCTGAGCCCATGATCCCGAGAGCGGAGCTGAGACGAGGCGGCGTGAAGTACGA 523
Db 428 GAGGTGAGAGAGATGATGAAGAAAGCATTTGATGATGATGATGATGATTAATGA 487
QY 524 GAGCTGCGGAGATGCT 541
Db 488 TGAATTTGTCAAGATGAT 505

RESULT 15

US-08-993-380-3
; Sequence 3, Application US/08993380B
; Patent No. 6077676
; GENERAL INFORMATION:
; APPLICANT: Sh. Qian-Li
; TITLE OF INVENTION: SINGLE CHAIN POLYPEPTIDES COMPRISING TROPONIN I AND
; FILE REFERENCE: 1112-1-053
; CURRENT APPLICATION NUMBER: US/08/993, 380B
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patent Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1173
; TYPE: DNA
; ORGANISM: Homo sapiens (modified)
US-08-993-380-3

Query Match 9.1%; Score 78.2; DB 3; Length 1173;
Best Local Similarity 53.3%; Pred. No. 3; 6e-07;
Matches 201; Conservative 0; Mismatches 158; Indels 18; Gaps 1;

QY 180 GATGAAGAGGACCATCAATGCCAGAGGCTGGGCGGCGGCTGAAGGCGGAGCA 239
Db 778 GCTGAGATGCTGATCAGCAGCAAGAGCTGGGCAAGATGATGATGATGATGATG 837
QY 240 AACCTTCGAGAGGCCACCTAAGAAACTCATCTCCAGGTTGACAGGAGCGGAGCGC 299
Db 838 AACCCACCCCTGAGAGAGCTGACAGAGATGATGATGATGATGATGATGATGATG 897
QY 300 GAAATCAGCTTCAGAGGTTCTGACAGCGCGCAAGAAAGGCGGCGGCT----- 352
Db 898 ACGGTGAGCTTGTATGATGATGATGATGATGATGATGATGATGATGATGATG 957
QY 353 -----GAGAGACCTGAGGCTGCTCCGCGCTTCGACCAAGATGAGGAGCGG 401
Db 958 GGAATTTGAGAGAGAGCTTCTGACCTCTTCCGATGTTTGAACAAATGCTGATG 1017
QY 402 CACATCAGCTGAGAGAGCTGAGCGGCGCATGAGCGGCGGCTGAGGAGCGGCGG 461
Db 1018 TACATGACCTGAGTATGATGATGATGATGATGATGATGATGATGATGATGAT 1077
QY 462 GAGAGCTGAGAGCGGATGATGATGATGATGATGATGATGATGATGATGATGAT 521
Db 1078 GACACATCAGAGAGCTTCAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1137
QY 522 GAGAGTTGCGGAGAT 538
Db 1138 GATGATGCTGAGATT 1154

Search completed: May 16, 2003, 01:36:21
Job time : 91 secs

score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

9214.099 million cell updates/sec

Sequence: 1 aattcccgatccctgcgc.....aggaatgcgagttccaaa 858

Scoring table: IDENTITY_NUC

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

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Minimum DB seq length: 0
Maximum DB seq length: 20000000000
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Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

GenEmb1: *

- 1: gb.ba: *
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- 5: gb.ov: *
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- 7: gb.ph: *
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- 9: gb.pr: *
- 10: gb.rst: *
- 11: gb.scs: *
- 12: gb.sy: *
- 13: gb.un: *
- 14: gb.vi: *
- 15: em.ba: *
- 16: em.fun: *
- 17: em.hum: *
- 18: em.in: *
- 19: em.mu: *
- 20: em.om: *
- 21: em.or: *
- 22: em.ov: *
- 23: em.pat: *
- 24: em.ph: *
- 25: em.pl: *
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- 29: em.vi: *
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- 32: em.hig_other: *
- 33: em.hig_rms: *
- 34: em.hig_pin: *
- 35: em.hic_rod: *
- 36: em.hic_nam: *
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- 38: em.sis: *
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Pred. No. is the number of results predicted by chance to have a

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3	843.4	98.5	913	6	AX399961	AX399961 Sequence
4	843.4	98.3	185926	2	AL732437	AL732437 Homo sapi
5	211.2	24.6	1306	6	AX333250	AX333250 Sequence
6	211.2	24.6	1306	6	AX334352	AX334352 Sequence
7	211.2	24.6	1306	6	AX335626	AX335626 Sequence
8	211.2	24.6	1306	9	HUMN1	MS8026.Human NB-1
9	211.2	24.6	1316	9	BC031889	BC031889 Homo sapi
10	211.2	24.6	2739	9	HUMCALP5	M676707 Human calmo
11	211.2	24.6	185926	2	AL732437	AL732437 Homo sapi
12	209.6	24.4	2746	6	AX335631	AX335631.Sequence
13	209.6	24.4	2746	6	HSCAMP5G	X134651 H.sapiens
14	185.4	21.6	106359	2	AC103443	AC103443 Rattus no
15	181.2	21.1	1519	3	MPCAM	hX5091 M. pyrifera
16	178.2	20.8	1111	3	TC0CALB2	X52096 Trypanosoma
17	174.6	20.3	899	10	AB036744	AB036744 Mus muscu
18	172.8	20.1	743	8	ZMRNRCAL	X74490 Z.mays MRNA
19	172.6	20.1	1358	8	PHITCALP1A	M63535 P. fiefestans
20	170.2	19.8	1439	7	BC005457	BC005457 Mus muscu
21	169.2	19.7	1357	3	AY118890	AY118890 Drosophila
22	169	19.7	824	8	AF042840	AF042840.Oryza sat
23	169	19.7	2175	9	HUMCAMA	Q40406 Human calmo
24	169	19.7	2190	7	BC005137	BC005137 Homo sapi
25	167	19.5	691	10	RSPRCM4	X13817 R.norvegicu
26	166.2	19.4	599	10	RATCAMB	M16659 Rat calmodu
27	166	19.3	450	5	ELCCALMA	M36168 E.electricu
28	166	19.3	883	5	ELCCAMEEL	X00931 E.electricu
29	165.4	19.3	542	8	AF007889	AF007889 Sybiodiod
30	165.4	19.3	616	3	LTCNAA	X80231 L.tarentola
31	165.2	19.3	722	10	MUSCALINDA	M19380 Mouse calmo
32	164.6	19.2	447	3	DMC4NR	Y00133 Drosophila
33	162.6	19.0	841	8	TAU45105	U9105 Trilicium ae
34	162.2	18.9	775	8	OSU7936	U7936 Oryza sativ
35	162.2	18.9	961	8	AF231026	AF231026 Oryza sat
36	161.6	18.8	480	8	AF031482	AF031482 Zea mays
37	159.6	18.6	1644	5	AF085250	AF085250 Perca fla
38	159.6	18.6	106359	2	AC103443	AC103443 Rattus no
39	158	18.4	450	5	CHKM11	K00510 Chicken CCM
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41	158	18.4	1038	3	BF133836	AJ133836 Branchios
42	157	18.3	1322	3	LR0291615	AJ291615 Lumbrios
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45	155.6	18.1	409	5	ORZCAMA	D10363 O. latipes

ALIGNMENTS

RESULT 1					
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DEFINITION	Sequence 2. from Patent WO0107604.				
ACCESSION	AX077138				
VERSION	AX077138.1	GI:13121753			
KEYWORDS					
SOURCE	human.				
ORGANISM	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
REFERENCE	1 (bases 1 to 858)				
AUTHORS	Mehul, B., Bernard, D. and Simonetti, L.				
TITLE	Isolated peptide of the horny layer and use thereof				
JOURNAL	Patent: WO 0107604-A 2 01-FEB-2001;				

OY	3	TTTCCGAGATCCCTGGGCTGGCTGCTCACTCTGAGACACAGGCTCTGAGAGCAGACAGTGTGA	62
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OY	63	GGGCGCGGTGGGACAGCTCGGAGAGCTCCGCGAGGTGAGAGACGACAGGCAATGGCCGGT	122
Db	111	GGGCGCGGTGGGACAGCTCGGAGAGCTCCGCGAGGTGAGAGACGACAGGCAATGGCCGGT	170
OY	123	GAGCTGACTCCTGAGAGAGAGAGGCCAGTACAAAAAGGCTTCTCCGGGTTGACACGGAT	182
Db	171	GAGCTGACTCCTGAGAGAGAGAGGCCAGTACAAAAAGGCTTCTCCGGGTTGACACGGAT	230
OY	183	GGAAACGGCGACCATCAATATGCGCCAGAGAGCTGGGCGCGGCGCTGAAGGCCACGGGCAAGAC	242
Db	231	GGAAACGGCGACCATCAATATGCGCCAGAGAGCTGGGCGCGGCGCTGAAGGCCACGGGCAAGAC	290
OY	243	CTCTCGGAGGCGCCAGCTTAAGAAACTCATCTCCAGAGTTGACAGGAGCGGCGGCGCA	302
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OY	303	ATCAGACTTCCACGAGATTCTGACGCGGCGCAAGAAAGCGCCAGGCGGCTGGAGAGACCTG	362
Db	351	ATCAGACTTCCAGAGATTCTGACGCGGCGCAAGAAAGCGCCAGGCGGCTGGAGAGACCTG	410
OY	363	CAGGTGCGCTTCCGCGCCTTGACACAGATGGCGGACGCGCCACATACCTGTGACGACGCTC	422
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Db	119	CCCTGGCATGGCCGACCGACAGCTGACTGAGGAGGAGGTCACAGATTCACAGAGAGGCTTCTC	178
QY	167	CGCGGTTGACACACGGATGAGAAACGGCACCATCATGATCCAGAGAGCTGGGCGCGGCTGAA	226
Db	179	CTGTATTGACAAAGATGGGAGACGGCTGCATCCACACCGGAGGCTGGGACAGTCATGGC	238
QY	227	GGCCACGGGGCAAGAACCTCTCTGGGAGGGCCAGCTAAGAGAACTCATCTCCGAGGTTGACAG	286
Db	239	GTCCTTGGGCCAGAAACCCACGGAGGCCGAGGTGGGGGACATGATGAGTGAATGACCG	298
QY	287	CGACGGCGACGGCGGAAATCAGCTTCCAGAGTTC-----TGAGGGGGGCAAGGA	337
Db	299	GGACGGCAACGGGACACCGTGGACTTCCCGGAGTCTCTGGGCATGATGGCCAGGAATGAA	358
QY	338	GGCCAGGGGCGGAGCTGAGAGACCTGCAGTGCCTTCGCGGCTTTCGACAGAGATGGGA	397
Db	359	GGACAGGGAACAAGAGAGAGAGATCCGGGAGGCTTCGCGGTTTCGACAGGAGCGGCA	418
QY	398	CGGCGCATCATCACCTGTGAGACGAGCTCAGGCGGGCCATGGCGGGGGCTGGGGGCAAGCTGCG	457
Db	419	CGGCTTCTCTCAGCGCGCGCGGAGCTACGACGTACGTAGACCGGGCTGGGGGGAACAACTGAG	478
QY	458	GCAGGAGAGAGCTGACAGGCGCATGATCCGGGAGGCGCCACAGTCGACAGAGCGGGGTTGA	517
Db	479	TGACAGAGAGAGGTGACAGAGATGATCCGGGCGCGGACACAGGAGAGAGGACGACAGTGA	538
QY	518	CTACAGAGAGTTCCGGAGAGATCTGCGCCAGAGTGAAGACTCCCGCGTGTGTCCCGTG	577
Db	539	CTACAGAGAGTTTGCCTGTGCTGTGTCACAAAGTAGAGGCGGCGCCACCATGTGCTCG	598
QY	578	GCTGCGCTCTAGGCTTTCAGGGCCACCGCCGCGTCC	613
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LOCUS	AX334352	1306 bp	DNA	linear	PAT 09-JAN-2002
DEFINITION	Sequence 4861 from Patent WO0194629.				
ACCESSION	AX334352				
VERSION	AX334352.1	GI:18125071			
KEYWORDS					
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
AUTHORS	1 Young, P.E., Augustus, M., Carter, K.C., Edner, R., Endress, G., Horigan, S., Soppet, D. R. and Weaver, Z.				
TITLE	Cancer gene determination and therapeutic screening using signature gene sets				
JOURNAL	Patent: WO 0194629-A 4861 13-DEC-2001;				
FEATURES	Avalon Pharmaceuticals (US)				
source	Location/Qualifiers				
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	/db_xref="taxon:9606"				
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ORIGIN					
Query Match	24.6%; Score 211.2; DB 6; Length 1306;				
Best Local Similarity	64.7%; Pred. No. 5.4e-20;				
Matches 334; Conservative	0; Mismatches 173; Indels 9; Gaps 1;				
OY	107 CGCAGCATGGCCGGTGAAGTCTGTCGAGGAGAGGCGCCAGTACAAAAGGCTTCTC.166				
Db	119 CCCTGGCATGGCGCGACACAGCTGATGAGGAGGAGCAGCAAGATTCAGAGAGCCCTTCTC.178				
OY	167 CGCGTTGACACAGCATGGAAGGCGACCATCATATGCCACAGAGCTGGGGCGGCGCTGAA.226				
Db	179 CCGTTGTTCAAGAGATGGGAGCGCTGCATCCACCGCGGAGCTGGGCGACGTCATGCG.238				

QY	227	GGCCACGGGGCAAGAACCTCTGGAGAGGCCAGCTAAGAAACATCTCCGAGGGTTGACAG	286
Db	239	GTCCCTGGGGCCAGAACCCACGAGAGGCCAGCTGGGGACATGATGAGTGAGANTGCACCG	298
QY	287	CGACGGCGACCGCGGAAATCAGCTTCCAGAGATTCC-----TGACGGGGCGCAAGGAA	337
Db	299	GGACGGCGAACCGCAACCGCTGGACCTTCCCGGAGTTCTGGGGCATGATGGCGCAGGAAGATTGA	358
QY	338	GGCCAGGGGCGCGCCCTGGAGGACCTGACAGTGGCTTCCCGGCGCTTTCGACAGAGATGGCGA	397
Db	359	GGACACGGGCAACGAGGAGGAGATCCGAGAGCCCTTCCGCGTGTTCGACAAAGAGAGCGCAA	418
QY	398	CGGCGACACTCAACCTGGAGCGAGCTCAGCGCGGGGCAATGGCGGGGCTGGGGGACCGGCTGCC	457
Db	419	CGGCTTCTGTTCAGCGCGCGCGGAGCTAAGCAGACGTCATGACACCGGGCTGGGGGGAAGACTGAG	478
QY	458	GCAGAGAGAGAGCTGACAGCGCATGATCCGAGAGGCCACATGACACAGAGACGGGCGGTTGAA	517
Db	479	TGACGAGGAGAGGTGGACGAGATGATCCGGGCGCGGACACGAGACGGGACAGGTGAA	538
QY	518	CTACGAGGAGTTCGCGGAGGATGCTCGCCACAGAGTGAAGGCTCCCGCGCTGTGTCTCCCTG	577
Db	539	CTACGAGGAGTGTTCCTCGTGTGTGTGTGTCCAAAGTGAAGCGCGGCGCCACCACTGTCCTG	598
QY	578	GCTGGCGCTCTGAGCCTTCAGGGGCCACCGCGCGGCTGC	613
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LOCUS	AX335626	1306 bp	DNA	Linear	PAT 09-JAN-2002
DEFINITION	Sequence 6135 from Patent WO0194629.				
ACCESSION	AX335626				
VERSION	AX335626.1	GI:18126345			
KEYWORDS					
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
AUTHORS	Young, P.E., Augustus, M., Carter, K.C., Ebner, R., Endress, G., Horriqan, S., Soppel, D.R. and Weaver, Z.				
TITLE	Cancer gene determination and therapeutic screening using signature gene sets				
JOURNAL	Patent: WO 0194629-A 6135 13-DEC-2001;				
FEATURES	Avalon Pharmaceuticals (US)				
Source	Location/Qualifiers				
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BASE COUNT	258 a	434 c	403 g	211 t	
ORIGIN					
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Best Local Similarity	64.7%	Pred. NO.5.4e-20;			
Matches 334;	Conservative	0;	Mismatches 173;	Indels	9; Gaps 1;
QY	107	CGCAGCGATGGCCGGCTGAGCTGACTGATCTCTCGAGGAGGAGGCCGCCAGTACAAAAAGCTTTCTC	166		
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QY	167	CGCGTTGACACGATGGAAAGCGACACCATCATATCCCAAGAGGCTGGGCGCGGCGCTGA	226		
Db	179	CCGTGTTGACAAAGGATGGGAGCGGCTGATCTACACCCCGCAGGCTGGCAGCGTTATCG	238		
QY	227	GGCCAGCGGCAAGAACTCTCGAGAGCCCACTTAAGAAACTCATCTCCGAGGTTGACAG	286		
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QY	287	CGACGGCGACGGCGCAATTCAGCTTCACAGAGTTCC-----TGACGGCGGCAAGAA	337		
Db	299	GGACGGCGCAAGCGACCGCTGAGACTTCCCGAGAGTCTTGGGCAATGATGGCGCAGGACATGAA	358		

QY 338 GCGCAGGCGCGGCTGAGAGCTGACGTCCTCCGCTTCGACAGAGATGCGCA 397
 Db 359 GGACACGCGACAAACGAGGAGAGATCCGCGAGGCTTCGCGCTGTTCAGACAGAGCGAA 418
 QY 398 CGGCGACATCAGCTGAGAGAGCTCAGGCGGCGCATGCGGCGGAGCCGCTGCC 457
 Db 419 CGGCTTGCTAGCGCCCGCGGCTACGACACGTCATGACCGCGCTGGGGAGAGCTGAG 478
 QY 458 GCAGAGAGCTGAGAGCGCATGATCCGCGAGCGGCGGAGAGAGAGAGAGAGAGAG 517
 Db 479 TGACGAGAGAGTGGACGAGATGATCCGCGCGGCGGACGAGAGAGAGAGAGAG 538
 QY 518 CTACGAGAGAGTTCGCGAGAGATGCTGCCAGAGAGTGAAGCTCCCGCTGTCTCCCTG 577
 Db 539 CTACGAGAGAGTTCGCGTGTGCTGTGTCCAGTGAAGCGCGCGCGCCACCATGCTCTG 598
 QY 578 GCTGCGCTGAGCGCTTCAGGCGGCGACCGCGCGCTGC 613
 Db 599 GCGCGCCACGCGGCGCCACAGGGCAAGAACCGGGGCG 634

RESULT 8

LOCUS HUMANB1 1306 bp mRNA linear PRI 27-Apr-1993
 DEFINITION Human NB-1 mRNA, complete cds.
 ACCESSION M58026
 VERSION M58026.1 GI:189080
 KEYWORDS NB-1.
 SOURCE Human breast epithelia cell, CDNA to mRNA.
 ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 AUTHORS Yaswen, P., Smoll, A., Peehl, D.M., Trask, D.K., Sager, R. and
 Stampfer, M.R.

TITLE Down-regulation of a calmodulin-related gene during transformation
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 87 (19), 7360-7364 (1990)
 MEDLINE 91017505
 PUBMED 2217169

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source location/Qualifiers
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BASE COUNT 258 a 434 c 403 g 211 t
 ORIGIN

Query Match 24.6%; Score 211.2; DB 9; Length 1306;
 Best Local Similarity 64.7%; Pred. No. 5.4e-20;
 Matches 334; Conservative 0; Mismatches 173; Indels 9; Gaps 1;

QY 107 CGCAGGATGCGCGTACTCTGAGAGAGAGCGCCAGTACAAAGAGCTTCTC 166
 Db 119 CCTCGGATGCGCCAGCAGCTGAGAGAGAGTCAAGAGAGAGAGCTTCTC 178
 QY 167 CGCGGTTGACAGGAGAAAGCGCACCATCAATGCCAGAGAGCTGGCGCGCTGAA 226
 Db 179 CCTGTTGACAAAGATGGGACGCGCTGATCACACCGGAGAGCTGGGACAGTATGCG 238
 QY 227 GCGCAGGCGCAAGAACTCTGCGAGAGCGCCAGCTAAGAAACTCATCTCCGAGTTGACAG 286

Db 239 GTCCCTGGCGCAGAACCCACAGAGGCGGAGCTCGGAGCATGATGATGATGATGACCG 298
 QY 287 CGAGCGCGCGGCAAAATACCTTCCAGAGAGTCC-----TGACGCGCGGCAAGAA 337
 Db 299 GGAGCGCAGCGGACACCGTGAATCCCGGAGTCTCTGGCATATGAGCAGAGAGAGAA 358
 QY 338 GCGCAGGCGCGGCTGAGAGCTGACAGATGCTCCGCGCTTCGACAGAGATGCGCA 397
 Db 359 GGACACGCGACAAACGAGGAGAGATCCGCGAGGCTTCGCGCTGTTCACAGAGAGCGAA 418
 QY 398 CGGCGACATCAGCTGAGAGCTCAGCGGCGCATGCGGCGGAGAGAGAGAGAGAG 457
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 QY 458 GCAGAGAGCTGAGAGCGCATGATCCGCGAGCGGCGGAGAGAGAGAGAGAGAGAG 517
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 Db 539 CTACGAGAGAGTTCGCGTGTGCTGTGTCCAGTGAAGCGCGCGCCACCATGCTCTG 598
 QY 578 GCTGCGCTGAGCGCTTCAGGCGGCGACCGCGCGCTGC 613
 Db 599 GCGCGCCACGCGGCGCCACAGGGCAAGAACCGGGGCG 634

RESULT 9

LOCUS BC031889 1316 bp mRNA linear PRI 27-JUN-2002
 DEFINITION Homo sapiens, calmodulin-like 3, clone MGC:30093 IMAGE:4777524,
 mRNA, complete cds.
 ACCESSION BC031889
 VERSION BC031889.1 GI:21619432
 KEYWORDS MGC.
 SOURCE human.
 ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 AUTHORS Strausberg, R.
 JOURNAL Direct Submission
 Submitted (06-JUN-2002) National Institutes of Health, Mammalian
 Gene Collection (MGC), Cancer Genomics Office, National Cancer
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
 USA

REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 CONTACT: MGC help desk
 Email: cgaps-remail.nih.gov
 Tissue Procurement: James Cleaver, M.D.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
 DNA Sequencing by: Baylor College of Medicine Human Genome
 Sequencing Center
 Center code: BCM-HGSC
 Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>
 Contact: amg@bcm.tmc.edu
 Guaratue, P.H., Garcia, A.M., Lu, X., Huiyk, S.W., Hale, S.M.,
 Yoon, V.S., Kovis, C.R., Lawrence, S., Martin, R.G., Muzny, D.M.,
 Richards, S., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/LNLN at: <http://image.llnl.gov>
 Series: IRAP Plate: 42 Row: e Column: 15
 This clone was selected for full length sequencing because it
 passed the following selection criteria: matched mRNA gi: 4885110.

FEATURES

source location/Qualifiers
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Db 1546 GGGCCCGACGGCCGACAGAGAGAACCCGGGGC 1581

RESULT 13
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LOCUS H.sapiens intronless calmodulin-like gene (CLP gene) for
DEFINITION calmodulin-like protein.
ACCESSION X13461
VERSION X13461.1 GI:29649
KEYWORDS calmodulin; calmodulin homologue.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 2739)
AUTHORS Koller, M. and Strehler, E.E.
TITLE Characterization of an intronless human calmodulin-like pseudogene
JOURNAL FEBS Lett. 239 (1), 121-128 (1988)
MEDLINE 89031205
PUBMED 3181418

REFERENCE 2 (bases 1 to 2746)
AUTHORS Koller, M.
TITLE Direct Submission
JOURNAL Submitted (14-MAY-1990) Koller M., Swiss Federal Institute of
Technology, Laboratory for Biochemistry III, ETH Zentrum,
Universitaetsstr. 16, CH-8092 Zurich, Switzerland
revised by [3]

REFERENCE 3 (bases 1 to 2746)
AUTHORS Koller, M.
TITLE Direct Submission
JOURNAL Submitted (08-JAN-1992)
REFERENCE 4 (bases 1 to 2746)
AUTHORS Koller, M. and Strehler, E.E.
TITLE Functional analysis of the promoters of the human CamIII calmodulin
gene and of the intronless gene coding for a calmodulin-like
protein
JOURNAL Biochim. Biophys. Acta 1163 (1), 1-9 (1993)
MEDLINE 93237314
PUBMED 8476923

FEATURES
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892..896
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ORIGIN

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Matches 333; Conservative 0; Mismatches 174; Indels 9; Gaps 1;

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DB 1066 CCTGTGATGCGCGACGAGTGAAGAGAGAGTCAAGATTCAGAGAGGCGCTTCTC 1125

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DB 1186 GTCCCTGGGCGCAAGCCACAGGAGCGGAGCTGGGGGACATGATGATGATGACG 1245

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DB 1246 GCACGCGCAACGCGACCGCTGAGATCTCCGAGTTCCTGGGCATGATGCGCAGCAATGTA 1305

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DB 1366 CGGCTTCGTCAGCGCGCGCGGACGCTCGACACGTCATGACCGCGCTGGGGAGAACTGAG 1425

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VERSION AC103443.3
KEYWORDS HTG; HTGS_PHASE1.
SOURCE Norway rat.
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Li, J., Li, Z., Lichtenarge, O., Lieu, C., Liu, J., Liu, W., Lounsged, H.,
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Unpublished
2 (bases 1 to 106359)
Morley, K.C.
Direct Submission
Submitted (25-NOV-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 106359)
Morley, K.C.
Direct Submission
Submitted (12-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Jul 11, 2002 this sequence version replaced gi:17973266.

----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GHOK
Center clone name: CH230-176G9
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Sequencing vector: Plasmid
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 53847 bases at least Q40
Consensus quality: 57227 bases at least Q30
Consensus quality: 60201 bases at least Q20

* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 57 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
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PI Mehul B, Bernard D, Simonetti L;
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 DR P-PSDB: AAB67650.
 XX New polypeptide isolated from human skin and having calcium fixing
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 PT differentiation, e.g. in treatment of dry skin, psoriasis or neoplasia
 PT
 PS Claim 17: Page 22; 28pp; French.
 XX
 CC The present sequence encodes a human calmodulin-like skin protein
 CC (CLSP). CLSP is a calcium-mediated signal pathway modulator. CLSP
 CC polypeptides and polynucleotides are used cosmetically for regulating
 CC dysfunction of epidermal proliferation or differentiation (normal or
 CC pathological) and for treating dry skin, hyperkeratosis, parakeratosis,
 CC psoriasis, ichthyosis or neoplasia. They are especially used for
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 DT 05-JUN-2002 (first entry)
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 KW hyperproliferative disorder; neoplasm; cardiovascular disease;
 KW cardiac arrest; cerebrovascular disorder; ischemia; angiogenesis;
 KW nervous system disorder; Alzheimer's disease; AIDS; ocular disorder;
 KW acquired immunodeficiency virus; dysphagia; gastrointestinal disorder;
 KW adenocarcinoma; reproductive system disorder; testicular feminisation;
 KW endocrine disorder; diabetes; cancer; leukemia; neovascularisation;
 KW respiratory disorder; renal disorder; kidney failure; blood disorder;
 KW myocardial infarction; wound healing; cell proliferation; skin aging;
 KW food additive; food preservative; gene therapy; gene; ss.
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 OS Homo sapiens.
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 PD 02-AUG-2001.
 XX
 PF 17-JAN-2001; 2001WO-US01332.
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 PR 04-FEB-2000; 2000US-0180628.
 PR 24-FEB-2000; 2000US-0184664.
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KW	fungicide; ophthalmological; cytostatic; immunosuppressive; nootropic;
KW	neuroprotective; antiallergic; hepatotropic; antidiabetic;
KW	antiinflammatory; anticancer; vulnery; anticonvulsant; antibacterial;
KW	antiparasitic; cardiac; gene therapy; cancer; immune disorder;
KW	cardiovascular disorder; neurological disease; infection; human; ss.
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PR 20-OCT-2000; 2000US-0241825.
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 PR 17-NOV-2000; 2000US-0249217.
 PR 17-NOV-2000; 2000US-0249218.
 PR 17-NOV-2000; 2000US-0249244.
 PR 17-NOV-2000; 2000US-0249245.
 PR 17-NOV-2000; 2000US-0249264.
 PR 17-NOV-2000; 2000US-0249265.
 PR 17-NOV-2000; 2000US-0249297.
 PR 17-NOV-2000; 2000US-0249299.
 PR 17-NOV-2000; 2000US-0249300.
 PR 01-DEC-2000; 2000US-0250160.
 PR 01-DEC-2000; 2000US-0250391.
 PR 05-DEC-2000; 2000US-0251030.
 PR 05-DEC-2000; 2000US-0251988.
 PR 05-DEC-2000; 2000US-0256719.
 PR 06-DEC-2000; 2000US-0251479.
 PR 08-DEC-2000; 2000US-0251856.
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 PR 11-DEC-2000; 2000US-0254097.
 PR 05-JAN-2001; 2001US-0259678.
 XX
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PJ Rosen CA, Barash SC, Ruben SM;
 XX
 DR WPI: 2001-488781/53.
 DR P-PSDB; AAM43627.
 XX
 PT New isolated nucleic acids and polypeptides, useful for diagnosing,
 XX treating and/or preventing human diseases and disorders -
 PS
 XX Claim 1: SEQ ID NO 141; 664bp + Sequence Listing; English.
 CC The invention relates to human polynucleotides (AA163803-AA164012) and
 CC the encoded proteins (AAM44497-AAM43660) useful for preventing, treating
 CC or ameliorating medical conditions e.g. by protein or gene therapy. The
 CC genes were isolated from a range of human tissues disclosed in the
 CC specification. The nucleic acids, proteins, antibodies and (ant)agonists
 CC are useful in the diagnosis, treatment and prevention of: (a) cancer,
 CC e.g. breast and ovarian cancer and other cancers of the adrenal gland,
 CC bone, bone marrow, breast, gastrointestinal tract, liver, lung, or
 CC urogenital; (b) immune disorders e.g. Addison's disease, allergies,
 CC autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus,

CC Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative
 CC colitis; (c) cardiovascular disorders such as myocardial ischaemias;
 CC (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and
 CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
 CC and parasitic infections.
 CC Note: The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 884 BP; 162 A; 273 C; 311 G; 135 T; 3 other;

Query Match 98.3%; Score 843.6; DB 22; Length 884;
 Best Local Similarity 98.8%; Pred. No. 2,5e-136;
 Matches 846; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

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 QY 63 GGGCCGGTGGGAGAGCAGCTCGAGGCTCCGAGGTGAGAGACGAGCATGGCGGT 122
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 QY 183 GGAACGAGCAGCATCATATCCCAAGAGCTGGGCGGCGCTGAAGGCCAGGCAAGAAC 242
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 QY 243 CTCTCGAGAGCCAGCTAAGAAATCATCTCGAGGTTGACAGCAGCGAGCGAGAA 302
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 QY 423 AGCGGGGAGGAGGCGGGGCTGGGAGCGGCTCCGAGAGAGAGCTGAGACGCGATGATC 482
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 DB 863 CTGCGAGTTCAGAAA 858

Db 864 CTGCCGACTCAAAA 879

RESULT 5
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ID AAS31614 standard; cDNA; 884 BP.
XX AAS31614;
AC
XX
DT 04-DEC-2001 (first entry)
XX
DE cDNA encoding novel human calcium-binding protein #38.
XX
KW Human; calcium-binding protein; calcium flux; neurological disease;
KW immune dysfunction; digestive disorder; neoplastic disease;
KW blood disorder; infectious disease; gene therapy; immunosuppressive;
KW antithrombotic; cytostatic; vasotropic; antibacterial; nootropic;
KW vitruclide; ss.
XX
OS Homo sapiens.
XX
PN W0200155304-A2.
XX
PD 02-AUG-2001.
XX
PE 17-JAN-2001; 2001WO-US01302.
XX
PR 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
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 PR 01-DEC-2000; 2000US-0250391.
 PR 05-DEC-2000; 2000US-0251030.
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 PR 08-DEC-2000; 2000US-0251868.
 PR 08-DEC-2000; 2000US-0251869.
 PR 08-DEC-2000; 2000US-0251989.
 PR 11-DEC-2000; 2000US-0254097.
 PR 05-JAN-2001; 2001US-0259678.
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 XX Rosen CA, Barash SC, Ruben SM;
 PI WPI: 2001-465568/50.
 XX P-PSDB: AAU19929.
 DR
 DR
 PT Isolated nucleic acid molecule encoding a calcium-binding protein is
 PT used in preventing, treating or ameliorating a medical condition -
 XX
 XX
 PS Claim 4; SEQ ID No 48; 542pp; English.
 XX
 XX The present invention relates to the isolation of novel human
 CC calcium-binding proteins (AAU19892-AAU19969), and cDNA and genomic
 CC sequences encoding for these proteins. The sequences of the invention
 CC are useful in the diagnosis, prevention and/or prognosis of diseases
 CC associated with aberrant calcium flux. Such disorders include
 CC neurological diseases (e.g. amyotrophic lateral sclerosis, ALS),
 CC immune dysfunction (e.g. severe combined immunodeficiency, SCID),
 CC digestive disorders (e.g. irritable bowel syndrome, IBS), neoplastic
 CC disease (e.g. cancer), blood disorders (e.g. haemophilia), and/or
 CC infectious disease (e.g. acquired immunodeficiency syndrome, AIDS). The
 CC novel calcium-binding proteins are also useful as screening tools to
 CC identify antagonists and/or agonists that may enhance or inhibit
 CC activities mediated by calcium-binding proteins. The polynucleotides of
 CC the invention are also useful in gene therapy. AAS31577-AAS31654
 CC represent cDNA sequences encoding for the novel human calcium-binding
 CC proteins.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at [ftp.wipo.int/pub/published_pct_sequences](http://wipo.int/pub/published_pct_sequences).
 CC
 XX
 SQ Sequence 884 BP; 162 A; 273 C; 311 G; 135 T; 3 other:
 Query Match 98.3%; Score 843.6; DB 22; Length 884;
 Best Local Similarity 98.8%; Pred. No. 2.5e-136;
 Matches 846; Conservative 3; Mismatches 7; Indels 0; Gaps 0;
 0y 3 TTCGGGATCCTGCGGCTGCTGACCTGACACGAGCTCTGAGAGAGAGTTGA 62
 Db 24 TCCCGGATCCTGCGGCTGCTGACCTGACACGAGCTCTGAGAGAGAGTTGA 83
 0y 63 GGGCGGTGGGAGAGAGCTCGGAGGCTCCGAGGTGACGAGACGACGATGGCCGT 122
 Db 84 GGGCGGTGGGAGAGAGCTCGGAGGCTCCGAGGTGACGAGACGACGATGGCCGT 143
 0y 123 GAGCTGACCTCTGAGAGAGAGCCAGTACAAAAGCTTTCTCCGGTTCACAGGAT 182
 Db 144 GAGCTGACCTCTGAGAGAGAGCCAGTACAAAAGCTTTCTCCGGTTCACAGGAT 203
 0y 183 GGAAGAGGACCATCAATCCAGAGAGCTGGGCGGCGCTCAAGGCGACGGCAAGAC 242
 Db 204 GGAAGAGGACCATCAATCCAGAGAGCTGGGCGGCGCTCAAGGCGACGGCAAGAC 263
 0y 243 CTCTCGAGAGCCCACTAAGAACTCATCTCCGAGGTTGACAGCGGCGAGCGAA 302

Db 264 CTCTCGAGAGCCAGCTAAGAACTCATCTCCGAGGTTGACAGCGGCGAGCGAA 323
 0y 303 ATCAGCTTCAGAGAGTTCTGTACGCGGCGCAGAGAGCGGCGCTGAGAGACTG 362
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 Db 384 CAGTGGCTTCGCGGCTTCGACACAGAGATGGGAGAGCGGCGCAGTACCGGTGAGAGCTC 443
 0y 423 AGCGGCGCATGCGGCGGCTGCGGCGAGCGGCTCCGAGAGAGAGTGAAGCATGATC 482
 Db 444 AGCGGCGCATGCGGCGGCTGCGGCGAGCGGCTCCGAGAGAGAGTGAAGCATGATC 503
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 AC
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 XX ABK43908;
 DT 05-JUN-2002 (first entry)
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 DE DNA encoding novel central nervous system protein #488.
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 XX Central nervous system; CNS; autoimmune disease; rheumatoid arthritis;
 KW hyperproliferative disorder; neoplasm; cardiovascular disorder;
 KW cardiac arrest; cerebrovascular disorder; ischemia; angiodysplasia;
 KW nervous system disorder; Alzheimer's disease; AIDS; ocular disorder;
 KW acquired immunodeficiency virus; dysphagia; gastrointestinal disorder;
 KW adenocarcinoma; reproductive system disorder; testicular feminisation;
 KW endocrine disorder; diabetes; cancer; leukaemia; neovascularisation;
 KW respiratory disorder; renal disorder; kidney failure; blood disorder;
 KW myocardial infarction; wound healing; cell proliferation; skin aging;
 KW food additive; food preservative; gene therapy; gene; ss.
 XX
 XX Homo sapiens.
 OS
 XX
 PN WO200155318-A2.
 XX
 XX 02-AUG-2001.
 XX
 XX 17-JAN-2001; 2001WO-US01332.
 PF
 XX

PR 31-JAN-2000; 2000US-0179065.
 PR 04-FEB-2000; 2000US-0180628.
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 PR 02-MAR-2000; 2000US-0186350.
 PR 16-MAR-2000; 2000US-0189874.
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 PR 19-MAY-2000; 2000US-0205515.
 PR 07-JUN-2000; 2000US-0209467.
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 PR 30-JUN-2000; 2000US-0215135.
 PR 07-JUL-2000; 2000US-0216647.
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 PR 08-NOV-2000; 2000US-0246475.
 PR 08-NOV-2000; 2000US-0246476.
 PR 08-NOV-2000; 2000US-0246477.
 PR 08-NOV-2000; 2000US-0246478.
 PR 08-NOV-2000; 2000US-0246523.
 PR 08-NOV-2000; 2000US-0246524.
 PR 08-NOV-2000; 2000US-0246525.
 PR 08-NOV-2000; 2000US-0246526.
 PR 08-NOV-2000; 2000US-0246527.
 PR 08-NOV-2000; 2000US-0246528.
 PR 08-NOV-2000; 2000US-0246532.
 PR 08-NOV-2000; 2000US-0246609.
 PR 08-NOV-2000; 2000US-0246610.
 PR 08-NOV-2000; 2000US-0246611.
 PR 08-NOV-2000; 2000US-0246613.
 PR 17-NOV-2000; 2000US-0249207.
 PR 17-NOV-2000; 2000US-0249208.
 PR 17-NOV-2000; 2000US-0249209.
 PR 17-NOV-2000; 2000US-0249210.
 PR 17-NOV-2000; 2000US-0249211.
 PR 17-NOV-2000; 2000US-0249212.
 PR 17-NOV-2000; 2000US-0249213.
 PR 17-NOV-2000; 2000US-0249214.
 PR 17-NOV-2000; 2000US-0249215.
 PR 17-NOV-2000; 2000US-0249216.
 PR 17-NOV-2000; 2000US-0249217.
 PR 17-NOV-2000; 2000US-0249218.
 PR 17-NOV-2000; 2000US-0249244.
 PR 17-NOV-2000; 2000US-0249245.
 PR 17-NOV-2000; 2000US-0249264.
 PR 17-NOV-2000; 2000US-0249265.
 PR 17-NOV-2000; 2000US-0249297.
 PR 17-NOV-2000; 2000US-0249299.
 PR 17-NOV-2000; 2000US-0249300.
 PR 01-DEC-2000; 2000US-0250160.
 PR 01-DEC-2000; 2000US-0250391.
 PR 05-DEC-2000; 2000US-0251030.
 PR 05-DEC-2000; 2000US-0251988.
 PR 05-DEC-2000; 2000US-0256719.
 PR 06-DEC-2000; 2000US-0251479.
 PR 08-DEC-2000; 2000US-0251856.
 PR 08-DEC-2000; 2000US-0251868.
 PR 08-DEC-2000; 2000US-0251869.
 PR 08-DEC-2000; 2000US-0251889.
 PR 08-DEC-2000; 2000US-0251990.
 PR 11-DEC-2000; 2000US-0254097.
 PR 05-JAN-2001; 2001US-0259678.

(HUMA-) HUMAN GENOME SCI INC.

Rosen CA, Barash SC, Ruben SM;

WPI; 2001-581633/65.
 P-PSDB; AA087578.

New isolated nucleic acid encoding a protein for diagnosing,
 preventing, treating or ameliorating medical conditions and used as

QY	3	TTCCCGGATCCCTCCGGCTGGCTGCATCTGAGGACACAGACCTCTGAAAGCAGCAGTTGA	62
Db	25	TGCCCCGATCCCTCCGGCTGCTTCACTCTTGACCAGAGCTCTGAGAGCAGCAGTTGA	84
QY	63	GGGCGGGTGGGCAAGCTCGGAGGCTCCGGAGGTCAGAGAGCGCAGGCATGCGCGT	122
Db	85	GGGCGGGTGGGCAAGCTCGGAGGCTCCGGAGGTCAGAGAGCGCAGGCATGCGCGT	144
QY	123	GAGCTGACTCCTGAGGAGGAGAGGCCCATACAAAAAGCCTTTCTCCGGGTTGACACGGAT	182
Db	145	GAGCTGACTCCTGAGGAGGAGAGGCCCATACAAAAAGCCTTTCTCCGGGTTGACACGGAT	204
QY	183	GGAACGGCAGCAGCAATATGCCCCAGAGAGCTGGGCGCGCGCTGGAAGGCGACGGGCAAAAC	242
Db	205	GGAACGGCAGCAGCAATATGCCCCAGAGAGCTGGGCGCGCGCTGGAAGGCGACGGGCAAAAC	264
QY	243	CTCTCGAGAGCCACAGCTAAGAAACTATCTCGAGGTTGACAGCGAGCGCGCGAA	302
Db	265	CTCTCGAGAGCCACAGCTAAGAAACTATCTCGAGGTTGACAGCGAGCGCGCGAA	324
QY	303	ATCAGCTTCCAGGAGTTCCTACAGGGCGCAAGGAAGCGCAGGGCGGGCTGAGAGACTG	362
Db	325	ATCAGCTTCCAGGAGTTCCTACAGGGCGGCRKRAAGGCGCAGGGCGGGCTGAGAGACTG	384
QY	363	CAGGTGCGCTTCGCGGCTTCGACAGAGATGGCGAGCGCCACATCACCGTGGAGAGACTC	422
Db	385	CANGTGCGCTTCGCGGCTTCGACAGAGATGGCGAGCGCCACATCACCGTGGAGAGACTC	444
QY	423	AGGCGGGCAGTGGGGGGGCTGGGGCAGC	450
Db	445	AGGCGGGCAGTGGGGGGGCTGGGGCAGC	472

RESULT 9	
AAC74951	
ID	MAC74951 standard; cDNA; 330 BP.
XX	
AC	
XX	AAC74951;
XX	
DT	08-FEB-2001 (first entry)
XX	
DE	Human ORFX ORF506 polynucleotide sequence SEQ ID NO:1011.
XX	
KW	Human; open reading frame; ORFX; detection; cytostatic; hepatotropic;
KW	vulnary; antipsoiatic; antiparkinsonian; neurotropic; neuroprotective;
KW	anticonvulsant; osteopathic; antiarthritis; immunosuppressant; cardiac;
KW	immunosuppressant; thrombolytic; coagulant; vasotropic; antidiabetic;
KW	hypotensive; dermatological; immunosuppressive; antiinflammatory;
KW	antiviral; antibacterial; antifungal; antirheumatic; antithyroid;
KW	antianemic; gene therapy; cancer; proliferative disorder; hypertension
KW	neurodegenerative disorder; osteoarthritis; graft vs host disease;
KW	cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;
KW	cholesterol ester storage; systemic lupus erythematosus; infection;
KW	severe combined immunodeficiency; malaria; autoimmune disorder; asthma;
KW	allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;
KW	bone damage; cartilage damage; antiinflammatory disease; coagulation;
KW	thrombosis; contraceptive; ss.
XX	
OS	Homo sapiens.
XX	
XX	MO200058473-A2.
XX	
PD	05-OCT-2000.
XX	
PF	31-MAR-2000; 2000MO-US08621.
XX	
PR	31-MAR-1999; 99US-0127607.
PR	02-APR-1999; 99US-0127636.
PR	05-APR-1999; 99US-0127728.
PR	30-MAR-2000; 2000US-0540763.
XX	
PA	(CURA-) CURAGEN CORP.

Query Match	Best Local Similarity	Matches	Conservative	Score	DB	Length	Indels	Gaps
3	99.38%	0	2	272.8	21	330	0	0
5	99.38%	0	2	236.38	38	330	0	0
6	99.38%	0	2	236.38	38	330	0	0
7	99.38%	0	2	236.38	38	330	0	0
8	99.38%	0	2	236.38	38	330	0	0
9	99.38%	0	2	236.38	38	330	0	0
10	99.38%	0	2	236.38	38	330	0	0
11	99.38%	0	2	236.38	38	330	0	0
12	99.38%	0	2	236.38	38	330	0	0
13	99.38%	0	2	236.38	38	330	0	0
14	99.38%	0	2	236.38	38	330	0	0
15	99.38%	0	2	236.38	38	330	0	0
16	99.38%	0	2	236.38	38	330	0	0
17	99.38%	0	2	236.38	38	330	0	0
18	99.38%	0	2	236.38	38	330	0	0
19	99.38%	0	2	236.38	38	330	0	0
20	99.38%	0	2	236.38	38	330	0	0
21	99.38%	0	2	236.38	38	330	0	0
22	99.38%	0	2	236.38	38	330	0	0
23	99.38%	0	2	236.38	38	330	0	0
24	99.38%	0	2	236.38	38	330	0	0
25	99.38%	0	2	236.38	38	330	0	0
26	99.38%	0	2	236.38	38	330	0	0
27	99.38%	0	2	236.38	38	330	0	0
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30	99.38%	0	2	236.38	38	330	0	0
31	99.38%	0	2	236.38	38	330	0	0
32	99.38%	0	2	236.38	38	330	0	0
33	99.38%	0	2	236.38	38	330	0	0
34	99.38%	0	2	236.38	38	330	0	0
35	99.38%	0	2	236.38	38	330	0	0
36	99.38%	0	2	236.38	38	330	0	0
37	99.38%	0	2	236.38	38	330	0	0
38	99.38%	0	2	236.38	38	330	0	0
39	99.38%	0	2	236.38	38	330	0	0
40	99.38%	0	2	236.38	38	330	0	0
41	99.38%	0	2	236.38	38	330	0	0
42	99.38%	0	2	236.38	38	330	0	0
43	99.38%	0	2	236.38	38	330	0	0
44	99.38%	0	2	236.38	38	330	0	0
45	99.38%	0	2	236.38	38	330	0	0
46	99.38%	0	2	236.38	38	330	0	0
47	99.38%	0	2	236.38	38	330	0	0
48	99.38%	0	2	236.38	38	330	0	0
49	99.38%	0	2	236.38	38	330	0	0
50	99.38%	0	2	236.38	38	330	0	0
51	99.38%	0	2	236.38	38	330	0	0
52	99.38%	0						

PR 05-JUN-2000; 2000US-209531P.
 PR 18-SEP-2000; 2000US-233133P.
 PR 18-SEP-2000; 2000US-233617P.
 PR 20-SEP-2000; 2000US-234009P.
 PR 20-SEP-2000; 2000US-234034P.
 PR 20-SEP-2000; 2000US-234052P.
 PR 22-SEP-2000; 2000US-234509P.
 PR 22-SEP-2000; 2000US-234567P.
 PR 25-SEP-2000; 2000US-234923P.
 PR 25-SEP-2000; 2000US-234924P.
 PR 25-SEP-2000; 2000US-235077P.
 PR 25-SEP-2000; 2000US-235082P.
 PR 25-SEP-2000; 2000US-235134P.
 PR 25-SEP-2000; 2000US-235280P.
 PR 26-SEP-2000; 2000US-235637P.
 PR 26-SEP-2000; 2000US-235638P.
 PR 27-SEP-2000; 2000US-235711P.
 PR 27-SEP-2000; 2000US-235720P.
 PR 27-SEP-2000; 2000US-235840P.
 PR 27-SEP-2000; 2000US-235863P.
 PR 28-SEP-2000; 2000US-236028P.
 PR 28-SEP-2000; 2000US-236032P.
 PR 28-SEP-2000; 2000US-236033P.
 PR 28-SEP-2000; 2000US-236034P.
 PR 28-SEP-2000; 2000US-236109P.
 PR 28-SEP-2000; 2000US-236111P.
 PR 29-SEP-2000; 2000US-236842P.
 PR 29-SEP-2000; 2000US-236891P.
 PR 02-OCT-2000; 2000US-237172P.
 PR 02-OCT-2000; 2000US-237173P.
 PR 02-OCT-2000; 2000US-237278P.
 PR 02-OCT-2000; 2000US-237294P.
 PR 02-OCT-2000; 2000US-237295P.
 PR 02-OCT-2000; 2000US-237316P.
 PR 03-OCT-2000; 2000US-237425P.
 PR 03-OCT-2000; 2000US-237598P.
 PR 03-OCT-2000; 2000US-237604P.
 PR 03-OCT-2000; 2000US-237606P.
 PR 03-OCT-2000; 2000US-237608P.
 PR 01-NOV-2000; 2000US-244867P.
 PR 01-NOV-2000; 2000US-245084P.
 PA (AVAL-) AVALON PHARM.
 XX
 XX
 PI Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;
 PI Soppet DR, Weaver Z;
 XX
 XX WPI: 2002-188264/24.
 XX
 PT Screening for anti-neoplastic agent involves exposing cells to a
 PT chemical agent to be tested for anti-neoplastic activity, and
 PT determining a change in expression of a gene of a signature gene set -
 XX
 PS Claim 1; SEQ ID 6135; 44pp; English.
 XX
 CC The present invention describes a method (M1) for screening for an
 CC anti-neoplastic agent. The method involves exposing cells to a chemical
 CC agent to be tested for anti-neoplastic activity, determining a change in
 CC expression of at least one gene (I) of a signature gene set, where (I)
 CC comprises a sequence (S) selected from 8447 sequences (given in ABL61664
 CC to ABL70110), or is at least 95% identical to (S), where a change in
 CC expression is indicative of anti-neoplastic activity. (I) has cycostatic
 CC activity and can be used in gene therapy. M1 can be used for screening
 CC an anti-neoplastic agent, and can be used for producing a product which
 CC is the data collected with respect to the anti-neoplastic agent as a
 CC structure and/or properties of the agent. M1 can be used in the
 CC treatment of cancer such as colon, breast, stomach, lung, thyroid,
 CC oesophageal, ovarian, kidney, prostate or pancreatic cancer,
 CC adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer,
 CC infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine
 CC carcinoma, papillary carcinoma and Wilm's tumour.
 XX

SO Sequence 1306 BP; 258 A; 434 C; 403 G; 211 T; 0 other:
 Query Match 24.6%; Score 211.2; DB 24; Length 1306;
 Best Local Similarity 64.7%; Pred. No. 8e-28;
 Matches 334; Conservative 0; Mismatches 173; Indels 9; Gaps 1;
 QY 107 CGCAGGATGCGCGGTGAGTCTGCTGCTGAGAGAGAGGCCAGTCAAAAAGCTTCTC 166
 Db 119 CCCTGGCATGGCGCACACGACTGAGGACAGTCAACAAATTCAGAGAGGCTTCTC 178
 QY 167 CGCGTTGACACAGATGGAACGACACATGATGCGAGGAGGCGGCGGCTTCTC 226
 Db 179 CCGTTTACAAAGATGGGAGCGGCTGCTGATCAACCGCGAGCTGGGACGCTCATGCG 238
 QY 227 GGCACAGGCAAGAACTCTGAGAGCCACCTAAGGAACATCTTCGAGTTGACAG 286
 Db 239 GTCCCTGGCCAGAACCCACGAGAGCGAGCTCGGGACATGATGATGATGATGACCG 298
 QY 287 CGACGGCGACGCGCAATCAGCTTCCAGAGATTCC-----TGACGGCGCAAGGA 337
 Db 299 GGACGGCAACGCGACCGTGGACTTCCGAGTCTCGGCATGATGGCGAGAGATGAA 358
 QY 338 GGCCAGGCGCGCGCTGAGAGACTGCAAGTCCGCGCTTCGACACAGATGGGA 397
 Db 359 GGACAGGCAACAGAGAGAGATCCGCGAGGCTTCCGCTGTTCCAAAGAGCGCA 418
 QY 398 CGGCCATCATCCGTGAGAGCTCAGCGGCGCATGGCGGGGCTGGGCGCGCTGCC 457
 Db 419 CGGCTTCGTACAGCGCCCGCCGAGTACGACATGCTACCGCGTGGGGAGAGCTGAG 478
 QY 458 GCAGAGAGAGTGGACCGCATGATCCCGAGAGCGGAGCTGACCAAGAGCGCGGGA 517
 Db 479 TGACAGAGAGTGGAGAGATGATCCGCGCGGAGGAGGAGAGAGAGAGTGA 538
 QY 518 CTACAGAGATTGCGAGAGATGCTGCGCCAGAGAGTGAAGCTCCCGCTGTCCCTG 577
 Db 539 CTAGAGAGATTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 598
 QY 578 GCTGCGCTGAGCTTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 613
 Db 599 GCGCGCCACGCGCGCCACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 634
 RESULT 13
 AA193552
 ID AA193552 standard; cDNA; 487 BP.
 XX
 XX
 AC AA193552;
 XX
 XX
 DT 06-NOV-2001 (first entry)
 XX
 DE Human polynucleotide SEQ ID NO 13612.
 XX
 KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
 KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
 KW tissue growth factor; immunomodulatory; cancer; leukaemia;
 KW nervous system disorders; arthritis; inflammation; ss.
 OS Homo sapiens.
 PN W0200164835-A2.
 XX
 XX 07-SEP-2001.
 PD 26-FEB-2001; 2001WO-US04927.
 PF 28-FEB-2000; 2000US-0515126.
 PR 18-MAY-2000; 2000US-0577409.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 XX Tang YT, Liu C, Dmanac RT;
 PI

DR WPI: 2001-514838/56.
 DR P-PSDB: AAO13621.
 PT Isolated nucleic acids and polypeptides, useful for preventing
 PT diagnosing and treating e.g. leukaemia, inflammation and immune
 PT disorders -
 XX
 PS Claim 1: SEQ ID NO 13612; 1399pp + Sequence listing; English.
 CC
 CC The invention relates to human polynucleotides (AA179941-AA193841) and
 CC the encoded proteins (AA000010-AA013910) that exhibit activity elating to
 CC cytokine, cell proliferation or cell differentiation or which may induce
 CC production of other cytokines in other cell populations. The
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
 CC peptide therapy. The polypeptides have various cytokine-like activities,
 CC e.g. stem cell growth factor activity, haematopoiesis regulating
 CC activity, tissue growth factor activity, immunomodulatory activity and
 CC activin/inhibin activity and may be useful in the diagnosis and/or
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
 CC inflammation.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pcr_sequences.
 CC
 XX Sequence 487 BP; 130 A; 104 C; 128 G; 105 T; 20 other:
 SQ
 Query Match 24.5%; Score 210.4; DB 22; Length 487;
 Best Local Similarity 96.4%; Pred. No. 1.2e-27;
 Matches 214; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
 OY 637 GGGAAACCTGCTGGTGGATGGAACCTGCTCCCTGGAGAGAGGCTTGGCGTCG 696
 DB 36 GGAATTCCTGCTGGTGGATGGAACCTGCTCCCTGGAGAGAGGCTTGGCGTCG 95
 OY 697 GGGCTGATGAGGGGGGCTCGGGGCTCGGAGGCTCTCTGCTCAAGACCTGGG 756
 DB 96 GGGCTGATGAGGGGGGCTCGGGGCTCGGAGGCTCTCTGCTCAAGACCTGGG 155
 OY 757 CAGAAGAGAGGCTCTGCTGGGCTGCTGCTTGGGCTGCTGATGAGAGGCTTGG 816
 DB 156 CAGAAGAGAGGCTCTGCTGGGCTGCTGCTTGGGCTGCTGATGAGAGGCTTGG 215
 OY 817 AACCCCGCATGATCTAAATAAAGAGCTCCGAGTTCAGAAA 858
 DB 216 ACCCCCGCATGATCTAAATAAAGAGCTCCGAGTTCAGAAA 257
 RESULT 14
 ABL67803
 ID ABL67803 standard; DNA; 2746 BP.
 XX
 AC ABL67803;
 XX
 DE 15-MAY-2002 (first entry)
 XX
 DE Oesophagus cancer related gene sequence SEQ ID NO:6140.
 XX
 KM Human: cancer: colon; breast; ovary; oesophagus; kidney; thyroid;
 KM stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
 KM cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
 KM gene; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO200194629-A2.
 XX
 PD 13-DEC-2001.
 XX
 PF 30-MAY-2001; 2001WO-US10838.
 XX
 PR 05-JUN-2000; 2000US-209473P.
 PR 05-JUN-2000; 2000US-209531P.
 PR 18-SEP-2000; 2000US-233133P.

PR 18-SEP-2000; 2000US-233617P.
 PR 20-SEP-2000; 2000US-234009P.
 PR 20-SEP-2000; 2000US-234034P.
 PR 20-SEP-2000; 2000US-234052P.
 PR 22-SEP-2000; 2000US-234509P.
 PR 22-SEP-2000; 2000US-234567P.
 PR 25-SEP-2000; 2000US-234923P.
 PR 25-SEP-2000; 2000US-234924P.
 PR 25-SEP-2000; 2000US-235077P.
 PR 25-SEP-2000; 2000US-235082P.
 PR 25-SEP-2000; 2000US-235134P.
 PR 25-SEP-2000; 2000US-235280P.
 PR 26-SEP-2000; 2000US-235637P.
 PR 26-SEP-2000; 2000US-235638P.
 PR 27-SEP-2000; 2000US-235711P.
 PR 27-SEP-2000; 2000US-235720P.
 PR 27-SEP-2000; 2000US-235840P.
 PR 27-SEP-2000; 2000US-235863P.
 PR 28-SEP-2000; 2000US-236028P.
 PR 28-SEP-2000; 2000US-236032P.
 PR 28-SEP-2000; 2000US-236033P.
 PR 28-SEP-2000; 2000US-236034P.
 PR 28-SEP-2000; 2000US-236109P.
 PR 28-SEP-2000; 2000US-236111P.
 PR 29-SEP-2000; 2000US-236842P.
 PR 29-SEP-2000; 2000US-236891P.
 PR 02-OCT-2000; 2000US-237172P.
 PR 02-OCT-2000; 2000US-237173P.
 PR 02-OCT-2000; 2000US-237278P.
 PR 02-OCT-2000; 2000US-237294P.
 PR 02-OCT-2000; 2000US-237295P.
 PR 02-OCT-2000; 2000US-237316P.
 PR 03-OCT-2000; 2000US-237425P.
 PR 03-OCT-2000; 2000US-237598P.
 PR 03-OCT-2000; 2000US-237604P.
 PR 03-OCT-2000; 2000US-237606P.
 PR 03-OCT-2000; 2000US-237608P.
 PR 01-NOV-2000; 2000US-244867P.
 PR 01-NOV-2000; 2000US-245084P.
 XX
 PA (AVAL-) AVALON PHARM.
 XX
 PI Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;
 PI Soppet DR, Weaver Z;
 XX
 DR WPI: 2002-188264/24.
 XX
 PT Screening for anti-neoplastic agent involves exposing cells to a
 PT chemical agent to be tested for anti-neoplastic activity, and
 PT determining a change in expression of a gene of a signature gene set -
 XX
 PS Claim 1: SEQ ID 6140; 44pp; English.
 XX
 CC The present invention describes a method (M1) for screening for an
 CC anti-neoplastic agent. The method involves exposing cells to a chemical
 CC agent to be tested for anti-neoplastic activity, determining a change in
 CC expression of at least one gene (I) of a signature gene set, where (I)
 CC comprises a sequence (S) selected from 8447 sequences (given in ABL61664
 CC to ABL70110), or is at least 95% identical to (S), where a change in
 CC expression is indicative of anti-neoplastic activity. (I) has cytoskeletal
 CC activity and can be used in gene therapy. M1 can be used for screening
 CC an anti-neoplastic agent, and can be used for producing a product which
 CC is the data collected with respect to the anti-neoplastic agent as a
 CC result of M1, and the data is sufficient to convey the chemical
 CC structure and/or properties of the agent. M1 can be used in the
 CC treatment of cancer such as colon, breast, stomach, lung, thyroid,
 CC oesophageal, ovarian, kidney, prostate or pancreatic cancer,
 CC adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer,
 CC infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine
 CC carcinoma, papillary carcinoma and Wilm's tumour.
 XX
 SQ Sequence 2746 BP; 590 A; 799 C; 801 G; 536 T; 0 other;

Query Match 24.4%; Score 209.6; DB: 24; Length 2746;
 Best Local Similarity 64.5%; Pred. No. 1.5e-27;
 Matches 333; Conservative 0; Mismatches 174; Indels 9; Gaps 1;

107 CGCAGGATGCGCGTGTGACTCTCTGAGAGAGGCGCCAGTACAAAGAGCTTCTC 166
 1066 CCTTGATGCGCGCGAGCTGAGTGTGAGGAGGAGTCAACAATTCAGAGAGCTTCTC 1125
 167 CGCGGTGACACGATGGAAGGCGACCATATATGCCCCAGAGAGCTGGCGCGCTGAA 226
 1126 CCTTTTGTACAGATGGGGAGGCTGTGATCACCACCGCGAGCTGGCGAGTCTATCG 1185
 227 GGGCAGGCGAAGACCTCTGAGAGCGCCAGTAAAGAACTCATCTCCAGGTTGAGAG 286
 1186 GTCCCTGGGCGAGAACCCACGAGAGGCGAGCTGGGACATGATGAGTGTGAGCG 1245
 287 CGACGGGACGCGCAATACCTTCAGAGAGTCC-----TGACGGCGGCAAGGAA 337
 1246 GGACGGGACGCGCACTTGGAGCTTCCCGAGTCTGTGATGAGGAGGAGATGAA 1305
 338 GGGCAGGCGCGCGCTGAGAGAGCTGAGAGTCCCTTCGCGCTTCAGCAGATGGCGA 397
 1306 GGACACGCGACACGAGAGGAGATCCGCGAGGCTTCGCGTTCGACAGAGAGCGCA 1365
 398 CGGCGACATCACGCTGAGACGAGCTCAGCGCGCATGGCGGCGCTGGGCGAGCGCTGCC 457
 1366 CGGCTGTGTACGCGCGCGCGAGCTGCGACGATGATGACCGGCTGGGCGAGAGCTGAG 1425
 458 GCAGGAGAGCTGAGACGCTGATCCGCGAGCGCGAGCTGAGAGCGAGCGGCTGAA 517
 1426 TGACGAGAGAGTGTGACGAGATGATCCGCGCGCGAGACGAGAGGAGAGAGTGA 1485
 518 CTACGAGAGTTCGCGAGAGATGCTGCCCGAGAGTGAAGCTCCCGCTGTGCTCCCTG 577
 1486 CTACGAGAGAGTTCGCTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1545
 578 GCTGCGCTGTGAGGCTTCAGAGGCGCACCGCGCGCTGC 613
 1546 GGGCGCGACGCGCGCGCACAGAGGCGCAAGAACCGGGGCG 1581

RESULT 15
 AAC03838
 ID AAC03838 standard; cDNA; 564 BP.
 XX
 AC AAC03838;
 XX
 DT 06-OCT-2000 (first entry)
 XX
 DE Human secreted protein 5' EST, SEQ ID NO: 3836.
 XX
 KM Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
 XX gene therapy; chromosome mapping; ss.
 OS Homo sapiens.
 XX
 PN EP1033401-A2.
 XX
 PD 06-SEP-2000.
 XX
 PF 21-FEB-2000; 2000EP-0200610.
 XX
 PR 26-FEB-1999; 99US-0122487.
 XX
 PA (GEST) GENSET.
 XX
 PI Dumas Milne Edwards J, Duclert A, Giordano J;
 XX
 DR WPI: 2000-500381/45.
 XX P-PSDB; AAG03832.
 XX
 PT New nucleic acid that is a 5' expressed sequence tag (5' EST) for
 PT obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for

PT diagnostic, forensic, gene therapy and chromosome mapping procedures -
 XX
 PS Claim 1; SEQ ID 3836; 71pp + CD-ROM; English.
 XX
 CC The present sequence is one of a large number of 5' ESTs derived from
 CC mRNAs encoding secreted proteins. An ORF has been identified within the
 CC sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs
 CC derived from 30 different tissues. EST sequences usually correspond
 CC mainly to the 3' untranslated region (UTR) of the mRNA because they are
 CC often obtained from oligo-dT primed cDNA libraries. Such ESTs are not
 CC well suited for isolating cDNA sequences derived from the 5' ends of
 CC mRNAs and even in those cases where longer cDNA sequences have been
 CC obtained, the full 5' UTR is rarely included. 5' ESTs are derived from
 CC mRNAs with intact 5' ends and can therefore be used to obtain full length
 CC cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic,
 CC gene therapy and chromosome mapping procedures. They are used to obtain
 CC upstream regulatory sequences and to design expression and secretion
 CC vectors.
 CC
 XX
 XX Sequence 564 BP; 146 A; 119 C; 191 G; 108 T; 0 other;

Query Match 19.8%; Score 170; DB: 21; Length 564;
 Best Local Similarity 62.3%; Pred. No. 9.8e-21;
 Matches 288; Conservative 0; Mismatches 165; Indels 9; Gaps 1;

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 54 AGGATGCTGTACACGCTGAGTGTGAGAGACAGATTGCAAGAGGCTTCTCCCT 113
 170 GGTGTACAGAGTGTGAAGAGGCGCACCATCATATGCCAGAGTGGCGCGCGCTGAAGGC 229
 114 CTTGTACAGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 173
 230 CACGCGCAAGAACCTTCGAGAGCGCCAGCTAAGAACTCATCTCCGAGTTGACAGCGA 289
 174 CCGTGTGAGAGAGAACCCACTGAAGAGAGCTGAGAGTGTGAGTGTGAGTGTGAGTGTG 233
 290 CGGCGAGCGCGCAATACCTTCGAGAGTCTCTGAGCGC-----GCAAGGAAGGC 340
 234 TGGAGAGCGGACATGTGACTTCCGAGGCTTCGACCATGATGCGCAAGAAAGATGAAGA 293
 341 CAGGCGCGCGCTGTGAGAGCTGTGAGAGTCCCTTCGCGCGCTTCGACGAGATGGCGAGG 400
 294 CACAGACAGTGTGAGAGAGATCCGAGAGGCTTCCGTGTCTTTGACAGAGATGGGAATGG 353
 401 CCACATCACCGTGTGAGAGAGCTCAGCGCGCGCATGCGCGCGCTGGGCGAGCGCTGCCGA 460
 354 CTACATCAGCGCGCGAGAGCTGCTGACATGATGACGAACCTGGGCGAGAGCTGACCGA 413
 461 GGAGAGCTGTGAGCGCATGATCCCGAGCGCGAGCTGAGACAGAGAGCGCGGTGAACCTA 520
 414 TGAGAGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 473
 521 CGAGAGTTCGCGAGAGTGTGCGCCAGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTG 562
 474 TGAAGAGTTGTACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 515

Search completed: May 15, 2003, 23:57:03
 Job time : 288 secs

GenCore version 5.1.4 p5.4578
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OM protein - nucleic search, using frame_plus_p2n model

Run on: May 16, 2003, 03:47:16 ; Search time 58 Seconds
(without alignments)
771.979 Million cell updates/sec

Title: US-10-031-403-1
Perfect score: 729
Sequence: 1 MAGELTPEEEHQYKKAFAV.....DVDQDGRVNYEFARMLAQE 146

Scoring table:
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Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-LOOPEXT=0 -UNITS=dits -START=1 -END=1 -MATRIX=Diosum62 -TRANS=human40.cdi
-LIST=45 -DOCALLIGN=200 -THR_SCORE=pcr -THR_MAX=100 -THR_MIN=0 -ALIGN=15
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-WARN_TIMCOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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5: /cgn2_6/ptodata/1/lna/PCVUS.COMB.seq:*
6: /cgn2_6/ptodata/1/lna/Backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	726	99.6	853	3	US-08-963-409-2
2	376.5	51.6	1929	2	US-08-818-253-1
3	376.5	51.6	1929	4	US-08-818-252-1
4	376.5	51.6	1929	2	US-08-818-252-1
5	376.5	51.6	1929	4	US-08-818-252-3
6	376.5	51.2	1929	2	US-08-818-252-3
7	373.5	51.2	1929	2	US-08-818-252-5
8	373.5	51.2	1971	4	US-08-818-252-7
9	373.5	51.2	1971	2	US-08-818-252-7
10	355.5	48.8	906	4	US-08-100-874-1
11	324.5	44.5	1401	1	US-09-239-909-1
12	305.5	41.9	916	4	US-09-239-909-3

13	286.5	39.3	1173	4	US-09-285-601-1	Sequence 1, Appl1
14	286.5	34.8	6709	2	US-09-285-601-3	Sequence 3, Appl1
15	254	39.8	836	4	US-08-698-805-7	Sequence 7, Appl1
16	239.5	32.9	1173	3	US-08-993-380-3	Sequence 3, Appl1
17	237.5	32.6	1349	1	US-07-951-715A-20	Sequence 20, Appl1
18	237.5	32.6	1349	2	US-08-459-448A-20	Sequence 20, Appl1
19	237.5	32.6	1349	3	US-08-459-595A-20	Sequence 20, Appl1
20	237.5	32.6	1349	3	US-08-459-504B-20	Sequence 20, Appl1
21	237.5	32.6	1349	3	US-08-459-444-20	Sequence 0, Appl1
22	237.5	32.6	1349	4	US-09-547-422-20	Sequence 7, Appl1
23	201.5	27.6	704	3	US-09-048-889-7	Sequence 7, Appl1
24	191	26.2	1400	1	US-08-464-164-1	Sequence 1, Appl1
25	191	26.2	1400	1	US-08-338-057-1	Sequence 1, Appl1
26	191	26.2	1400	2	US-08-668-416-1	Sequence 1, Appl1
27	171.5	23.5	944	1	US-08-468-855-3	Sequence 3, Appl1
28	171.5	23.5	944	1	US-08-468-855-3	Sequence 3, Appl1
29	171.5	23.5	944	1	US-08-310-357-3	Sequence 3, Appl1
30	171.5	23.5	944	1	US-08-468-855-3	Sequence 3, Appl1
31	171.5	23.5	944	2	US-08-468-857-3	Sequence 3, Appl1
32	158.5	21.7	839	1	US-08-884-682-2	Sequence 2, Appl1
33	158.5	21.7	839	2	US-09-096-082-2	Sequence 2, Appl1
34	156	21.4	524	1	US-08-328-322-16	Sequence 16, Appl1
35	156	21.4	812	1	US-08-328-322-13	Sequence 13, Appl1
36	151	20.7	420	4	US-09-641-638-584	Sequence 229, App
37	144	19.8	463	4	US-09-641-638-229	Sequence 584, App
38	144	19.8	464	4	US-09-641-638-234	Sequence 234, App
39	144	19.8	464	4	US-09-641-638-235	Sequence 235, App
40	138.5	19.0	439	4	US-09-641-638-240	Sequence 240, App
41	138.5	19.0	611	4	US-09-328-111-527	Sequence 527, App
42	138	18.9	420	4	US-09-641-638-227	Sequence 227, App
43	136.5	18.7	439	4	US-09-641-638-241	Sequence 241, App
44	136.5	18.7	439	4	US-09-641-638-242	Sequence 242, App
45	124	17.0	1055	2	US-08-828-242-2	Sequence 2, Appl1

ALIGNMENTS

RESULT 1
US-08-963-409-2
Sequence 2, Application US/08963409
Patent No. 6046315

GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Shah, Purvi
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: DISEASE ASSOCIATED CALMODULIN PROTEIN
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESS: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/963,409
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0418 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 853 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 IMMEDIATE SOURCE:
 LIBRARY: BRSTTUT14
 CLONE: 2743380
 US-08-963-409-2

Alignment Scores:

Pred. No.: 2,62e-81 Length: 853
 Score: 726.00 Matches: 145
 Percent Similarity: 100.00% Conservative: 1
 Best Local Similarity: 99.32% Mismatches: 0
 Query Match: 99.59% Indels: 0
 Gaps: 3

US-10-031-403-1 (1-146) x US-08-963-409-2 (1-853)

QY 1 MetAlaGlyLeuThrProGluGluAlaGlnTyrLysAlaPheSerAlaVal 20
 Db 121 ATGGCCGAGTACGCTGCTGAGAGAGAGGCCAGTACAAAAGCCTTCTCCGCGGT 180
 QY 21 AspThrAspGlyAsnGlyThrIleAsnAlaGlnGluLeuGlyAlaIleuLysAlaThr 40
 Db 181 GACACGATGGAAGGCGCACCATCATGCCAGAGCTGGCGGCGCTGAAGGCCACG 240
 QY 41 GlyLysAsnLeuSerGluAlaGlnLeuArgLysLeuIleSerGluValAspSerAspGly 60
 Db 241 GGCAAGAACTCTCGAGGCGGCGCAAGTAAAGAACTCATCTCCGAGGTGACAGGAGCGC 300
 QY 61 AspGlyLysLeuSerPheGlnGluPheLeuThrAlaAlaArgLysAlaArgAlaGlyLeu 80
 Db 301 GACGGCCAAATCAAGCTTCCAGAGTTCTCTACGCGCGCAAGAGCGCGCGCGCTG 360
 QY 81 GluAspLeuGlnValAlaPheArgAlaPheAspGlnAspGlyHisIleThrVal 100
 Db 361 GAGACCTGCAAGTGGCTTCTCCGCGCTTCCAGCAGAGTGGCGGCGCCATCACCGTG 420
 QY 101 AspGluLeuArgArgAlaMetAlaGlyLeuGlyGlnProLeuProGlnGluLeuAsp 120
 Db 421 GAGCAGCTCAGGGGCGGCGCATGGGCGGCTGGGAGCGCGCTGCCGCGAGAGAGCTGAC 480
 QY 121 AlaMetIleArgGluAlaAspValAspGlnAspGlyArgValAsnTyrGluGluPheAla 140
 Db 481 GCATGATCCGCGAGCGCGAGCTGACAGCAGCGGCGGCTGAACCTACGAGAGTTGCGC 540
 QY 141 ArgMetLeuAlaGlnGlu 146
 Db 541 AGCATGCTGCCCAAGAG 558

RESULT 2

US-08-818-253-1
 ; Sequence 1, Application US/08818253
 ; Patent No. 5998204

GENERAL INFORMATION:

APPLICANT: Tsien, Roger Y.
 TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR
 NUMBER OF SEQUENCES: 61
 CORRESPONDENCE ADDRESS:
 ADDRESSER: Fish & Richardson P.C.
 STREET: 4225 Executive Square, Suite 1400
 CITY: La Jolla
 STATE: CA
 COUNTRY: USA
 ZIP: 92037

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: Windows 95

SOFTWARE: FASTSEQ for Windows Version 2.0b

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/818,253
 FILING DATE: 14-MAR-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Hallie, Ph.D., Lisa A.

REGISTRATION NUMBER: 38,347

REFERENCE/DOCKET NUMBER: 07257/043001

TELECOMMUNICATION INFORMATION:

TELEPHONE: 619/678-5070

TELEFAX: 619/678-5099

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 1929 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

FEATURE:

NAME/KEY: Coding Sequence

LOCATION: 1..1926

US-08-818-253-1

Alignment Scores:

Pred. No.: 1.97e-37 Length: 1929
 Score: 376.50 Matches: 75
 Percent Similarity: 73.29% Conservative: 32
 Best Local Similarity: 51.37% Mismatches: 36
 Query Match: 51.65% Indels: 3
 Gaps: 2

US-10-031-403-1 (1-146) x US-08-818-253-1 (1-1929)

QY 1 MetAlaGlyLeuThrProGluGluAlaGlnTyrLysAlaPheSerAlaVal 20
 Db 688 ATGATGCAACCAAGTGAAGAGAGAGTTCAGAGTTCAAAAGAGCTTCTCATTTATTC 747
 QY 21 AspThrAspGlyAsnGlyThrIleAsnAlaGlnGluLeuGlyAlaIleuLysAlaThr 40
 Db 748 GACAAGATGAGGCGGCGCACCATTCACCAAGAACTTGGCAGCCGTTATGAGTCTCT 807
 QY 41 GlyLysAsnLeuSerGluAlaGlnLeuArgLysLeuIleSerGluValAspSerAspGly 60
 Db 808 GACAAACCAACCAAGCAGAGCAAGATTCAGAGTATGATCAATGAAGTCGATGATGC 867
 QY 61 AspGlyLysLeuSerPheGlnGluPheLeuThrAlaAlaArgLysAlaArg----- 77
 Db 868 AATGGAACGATTTACTTCTGAAATTTCTTACTATGATGCTGAGAAAATGAAGACACA 927
 QY 78 AlaGlyLeuGluAspLeuGlnValAlaPheArgAlaPheAspGlnAspGlyHis 97
 Db 928 GACAGCGAAGAGAAATCCGAGAAAGCATTCGCTTTTACAAAGATGGGAAGCGCTAC 987
 QY 98 IleThrValAspGluLeuArgArgAlaMetAlaGlyLeuGlyGlnProLeuProGlnGlu 117
 Db 988 ATCAGCCCTCTGATATTCATCTACGTCATGACAAACCTCGGCGGAGGATTAACAGATGA 1047
 QY 118 GluLeuAspAlaMetIleArgGluAlaAspValAspGlnAspGlyArgValAsnTyrGlu 137
 Db 1048 GAAGTTGATGAATGATTAAGGAGAGAGATGATGATGATGATGATGATGATGATGATGAA 1107
 QY 138 GluPheAlaArgMetLeu 143
 Db 1108 GAGTTTGTACAAATGATG 1125

RESULT 3

US-08-818-252-1
 ; Sequence 1, Application US/08818252B
 ; Patent No. 6197928
 ; GENERAL INFORMATION:

Db 1108 GAGTTGTACAAATGATG 1125
 RESULT 5
 US-08-818-252-3
 ; Sequence 3, Application US/08818252B
 ; Patent No. 6197928
 ; GENERAL INFORMATION:
 ; APPLICANT: Tsien, Roger Y.
 ; APPLICANT: Miyawaki, Atsushi
 ; TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR
 ; TITLE OF INVENTION: DETECTION OF ANALYTES
 ; FILE REFERENCE: 07257/042001
 ; CURRENT APPLICATION NUMBER: US/08/818, 252B
 ; CURRENT FILING DATE: 1997-03-14
 ; NUMBER OF SEQ ID NOS: 56
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 3
 ; LENGTH: 1959
 ; TYPE: DNA
 ; ORGANISM: Aequorea victoria
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (0)...(1956)
 US-08-818-252-3

Alignment Scores:
 Pred. No.: 2,01e-37 Length: 1959
 Score: 376.50 Matches: 75
 Percent Similarity: 73.29% Conservative: 32
 Best Local Similarity: 51.37% Mismatches: 36
 Query Match: 51.65% Indels: 3
 Gaps: 2

US-10-031-403-1 (1-146) x US-08-818-252-3 (1-1959)

QY 1 MetAlaGlyLeuThrProGluGluAlaGlnIleuTyrsAlaPheSerAlaVal 20
 Db 688 ATGATGATGACCACTGACGAGAGAGACAGATTGCGAGTTCAAGAGCTCTCTATTATTC 747
 QY 21 AspThrAspGlyAsnGlyThrIleAsnAlaGlnLeuGluAlaAlaLeuValaThr 40
 Db 748 GACAAGATGGGGAGCGGCACCATCCACCAAGAACTTGGACCCGTATGAGTCCCTT 807
 QY 41 GlyLysAsnLeuSerGluAlaGlnLeuArgLysLeuIleSerGluValaAspSerAspGly 60
 Db 808 GGCACAAACCCCAACGAGAGAGATTCAGATGATGATCAATGAACTCGATGATGCG 867
 QY 61 AspGlyCylLeuIleSerPheGlnGluPheLeuThr--AlaAlaArgLysAlaArg----- 77
 Db 868 AATGGAAACGATTACTTCTGTAATTTCTTACTGTATGATGCTGCAAAAATGAAGACACACA 927
 QY 78 AlaGlyLeuGluAspLeuGlnValaAlaPheArgAlaPheAspGlnAspGlyAspGlyHis 97
 Db 928 GACAGCGAAGAGAAATCCGAGAACATTCGCGTGTTCGACAAGATGGGAACGCTAC 987
 QY 98 IleThrValAspGluLeuArgArgAlaMetAlaGlyLeuGlnProLeuProGlnGlu 117
 Db 988 ATCAGCGCTCTGTAATTTACTGCTACGTCATGACAAACCTCGGGGAGATTAAACAGATGAA 1047
 QY 118 GluLeuAspAlaMetIleArgGluAlaAspValaAspGlnAspGlyAspGlyValaAspGly 137
 Db 1048 GAAGTTGATCAAAATGATTAAGGAGCAAGATATGATGATGCGCAAGTAACATATGAA 1107
 QY 138 GluPheAlaArgMetLeu 143
 Db 1108 GAGTTGTACAAATGATG 1125

RESULT 6
 US-08-818-253-5
 ; Sequence 5, Application US/08818253
 ; Patent No. 5998204
 ; GENERAL INFORMATION:

APPLICANT: Tsien, Roger Y.
 APPLICANT: Miyawaki, Atsushi
 TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR
 TITLE OF INVENTION: DETECTION OF ANALYTES
 NUMBER OF SEQUENCES: 61
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Fish & Richardson P.C.
 STREET: 4225 Executive Square, Suite 1400
 CITY: La Jolla
 STATE: CA
 COUNTRY: USA
 ZIP: 92037
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: Windows 95
 SOFTWARE: FastSeq for Windows Version 2.0b
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/818, 253
 FILING DATE: 14-MAR-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Hallie, Ph.D., Lisa A.
 REGISTRATION NUMBER: 38,347
 REFERENCE/DOCKET NUMBER: 07257/043001
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 619/678-5070
 TELEFAX: 619/678-5099
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1929 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 FEATURE:
 NAME/KEY: Coding Sequence
 LOCATION: 1...1926
 US-08-818-253-5

Alignment Scores:
 Pred. No.: 4.65e-37 Length: 1929
 Score: 373.50 Matches: 74
 Percent Similarity: 73.29% Conservative: 33
 Best Local Similarity: 50.68% Mismatches: 36
 Query Match: 51.23% Indels: 3
 Gaps: 2

US-10-031-403-1 (1-146) x US-08-818-253-5 (1-1929)

QY 1 MetAlaGlyLeuThrProGluGluAlaGlnIleuTyrsAlaPheSerAlaVal 20
 Db 688 ATGATGATGACCACTGACGAGAGAGACAGATTGCGAGTTCAAGAGCTCTCTATTATTC 747
 QY 21 AspThrAspGlyAsnGlyThrIleAsnAlaGlnLeuGluAlaAlaLeuValaThr 40
 Db 748 GACAAGATGGGGAGCGGCACCATCCACCAAGAACTTGGACCCGTATGAGTCCCTT 807
 QY 41 GlyLysAsnLeuSerGluAlaGlnLeuArgLysLeuIleSerGluValaAspSerAspGly 60
 Db 808 GGCACAAACCCCAACGAGAGAGATTCAGATGATGATCAATGAACTCGATGATGCG 867
 QY 61 AspGlyCylLeuIleSerPheGlnGluPheLeuThr--AlaAlaArgLysAlaArg----- 77
 Db 868 AATGGAAACGATTACTTCTGTAATTTCTTACTGTATGATGCTGCAAAAATGAAGACACACA 927
 QY 78 AlaGlyLeuGluAspLeuGlnValaAlaPheArgAlaPheAspGlnAspGlyAspGlyHis 97
 Db 928 GACAGCGAAGAGAAATCCGAGAACATTCGCGTGTTCGACAAGATGGGAACGCTAC 987
 QY 98 IleThrValAspGluLeuArgArgAlaMetAlaGlyLeuGlnProLeuProGlnGlu 117

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Db 988 ATCAGCCGCTGCTACGTACCTGACCAACCTCGGAGGAGATTACAGATGAA 1047
Oy 118 GluLeuAspAlaMetIleArgGlnAlaAspValaAspGlnAspGlyArgValaAsnTyrGlu 137
Db 1048 GAAAGTGTGAATAATGAAGGAGACAGATATGATGTGGCCAGTAAGTAACTATGAA 1107
Oy 138 GlupheaAlaArgMetLeu 143
Db 1108 GAGTTTGTACAAATGATG 1125

RESULT 7
US-08-818-252-5
; Sequence 5, Application US/08818252B
; Patent No. 6197928
; GENERAL INFORMATION:
; APPLICANT: Tsien, Roger Y.
; APPLICANT: Miyawaki, Atsushi
; TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR
; TITLE OF INVENTION: DETECTION OF ANALYTES
; FILE REFERENCE: 07257/042001
; CURRENT APPLICATION NUMBER: US/08/818,252B
; CURRENT FILING DATE: 1997-03-14
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 1929
; TYPE: DNA
; ORGANISM: Aequorea victoria
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (0)...(1926)
US-08-818-252-5

Alignment Scores:
Pred. No.: 4,65e-37 Length: 1929
Score: 373.50 Matches: 74
Percent Similarity: 73.29% Conservative: 33
Best Local Similarity: 50.68% Mismatches: 36
Query Match: 51.23% Indels: 3
DB: 4 Gaps: 2

US-10-031-403-1 (1-146) x US-08-818-252-5 (1-1929)
Oy 1 MetalaglyGluLeuThrProGlnGluAlaGlnTyrLysAlaPheSerAlaVal 20
Db 688 ATGCATGACCACTGACAGACAGATTCGACAGCTTCACATTTATTC 747
Oy 21 AspThrAspGlyAsnGlyThrIleAsnAlaGlnGluLeuGlyAlaAlaLeuLysAlaThr 40
Db 748 GACAAGGATGGGAGCGGCACCATCCACCAAGGAAGCACTTGCGATTGAGTGGCTT 807
Oy 41 GlyLysAsnLeuSerGlnAlaGlnLeuArgLysLeuIleSerGlnValaLysPheAspGly 60
Db 808 GGACAAACCCCAACGAGCAGCAATTCGATGATCAATGAAGTCACTGATGCGC 867
Oy 61 AspGlyGluIleSerPheGlnGluPheLeuThr---AlaAlaArgLysAlaArg----- 77
Db 868 AATGAGACGATTACTTCTTCCTCAATTTCTTACTATGATGGCTAGAAATAATGAGGACACA 927
Oy 78 AlaGlyLeuGluAspLeuGlnValaAlaPheArgAlaPheAspGlnAspGlyAsnTyrHis 97
Db 928 GACACGAGAAAGAGAAATCGAGACATTCGCTGTTTTCACAAGATGGAAGCGCTAC 987
Oy 98 IleThrValaAspGluLeuArgArgAlaMetAlaGlyLeuGlyGlnProLeuProGlnGlu 117
Db 988 ATCAGCCGCTGCTACGTACGTCATGACCAACCTCGGAGAGAAAGTTAACAGATGAA 1047
Oy 118 GluLeuAspAlaMetIleArgGlnAlaAspValaAspGlnAspGlyArgValaAsnTyrGlu 137
Db 1048 GAAAGTGTGAATAATGAAGGAGACAGATATGATGTGGCCAGTAACTATGAA 1107
Oy 138 GlupheaAlaArgMetLeu 143

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Db 1108 GAGTTTGTACAAATGATG 1125

RESULT 8
US-08-818-253-7
; Sequence 7, Application US/08818253
; Patent No. 5998204
; GENERAL INFORMATION:
; APPLICANT: Tsien, Roger Y.
; APPLICANT: Miyawaki, Atsushi
; TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR
; TITLE OF INVENTION: DETECTION OF ANALYTES
; NUMBER OF SEQUENCES: 61
; CORRESPONDENCE ADDRESS:
; ADDRESS: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/818,253
; FILING DATE: 14-MAR-1997
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Ph.D., Lisa A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 07257/043001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1971 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 1...1968
US-08-818-253-7

Alignment Scores:
Pred. No.: 4,79e-37 Length: 1971
Score: 373.50 Matches: 74
Percent Similarity: 73.29% Conservative: 33
Best Local Similarity: 50.68% Mismatches: 36
Query Match: 51.23% Indels: 3
DB: 2 Gaps: 2

US-10-031-403-1 (1-146) x US-08-818-253-7 (1-1971)
Oy 1 MetalaglyGluLeuThrProGlnGluAlaGlnTyrLysAlaPheSerAlaVal 20
Db 736 ATGCATGACCACTGACAGACAGATTCGACAGCTTCACAAAGACCTTCATTTATTC 795
Oy 21 AspThrAspGlyAsnGlyThrIleAsnAlaGlnGluLeuGlyAlaAlaLeuLysAlaThr 40
Db 796 GACAAGGATGGGAGCGGCACCATCCACCAAGGAAGCACTTGCGATTGAGTGGCTT 855
Oy 41 GlyLysAsnLeuSerGlnAlaGlnLeuArgLysLeuIleSerGlnValaLysPheAspGly 60
Db 856 GGACAAACCCCAACGAGCAGCAATTCGATGATCAATGAAGTCACTGATGCGC 915
Oy 61 AspGlyGluIleSerPheGlnGluPheLeuThr---AlaAlaArgLysAlaArg----- 77

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Db 916 AATGGAAGATTTACTTCTGAAATTTCTTACTTGATGGCTAGAGAAAATAGAGACACA 975
OY 78 AlaglyleugluaspLeugluValAlaPheArGAlaPheaspGlnaspGlyAspGlyHis 97
Db 976 GACAGCAGAGAGAAATCCGAGAGACATTCGCTGTTTGGACAGAGATGGAGAGGGCTAC 1035
OY 98 IlePheValaspGluLeuArGArGAlaMetAlaGlyLeuglyGlnProLeuProGlnGlu 117
Db 1036 ATCAGCCGCTGCTCAGTTACGTCACGTCACAAACCTCGGGGAGAGTTAACAGATGAA 1095
OY 118 GluLeuaspAlaMetIleArGAlaValaspAlaaspGlnaspGlyArGValaspGlyGlu 137
Db 1096 GAAGTTGATGAATAGTAAGAGAGAGATATCATGTGATGCGCAAGTAATATGAA 1155
OY 138 GluPheAlaArGMetLeu 143
Db 1156 GAGTTTGTACAAATGATG 1173

RESULT 9

US-08-818-252-7
; Sequence 7, Application US/08818252B
; Patent No. 6197928
; GENERAL INFORMATION:
; APPLICANT: Tsien, Roger Y.
; APPLICANT: Miyawaki, Atsushi
; TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR
; FILE REFERENCE: 07257/042001
; CURRENT APPLICATION NUMBER: US/08/818,252B
; CURRENT FILING DATE: 1997-03-14
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 1971
; TYPE: DNA
; ORGANISM: Aequorea victoria
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (0)...(1968)
US-08-818-252-7

Alignment Scores:
Pred. No.: 4,79e-37 Length: 1971
Score: 373.50 Matches: 74
Percent Similarity: 73.298 Conservative: 33
Best Local Similarity: 50.688 Mismatches: 36
Query Match: 51.238 Indels: 3
DB: 4 Gaps: 2

US-10-031-403-1 (1-146) x US-08-818-252-7 (1-1971)

OY 1 MetAlaGlyLeuLeuThrProGluGluGluAlaGlnTyrLysLysAlaPheSerAlaVal 20
Db 736 ATGCAATGACCACTGACAGAGAGAGATTCAGAGTTCAAGAGCCTCTCATTTATTC 795
OY 21 AspThrAspGlyAsnGlyThrIleAsnAlaGlnLeuGluValAlaLeuLysAlaThr 40
Db 796 GACAAGATGGAGCGCACCATCACCAAGAGAACTTGACCCGTTATGAGGTGCTT 855
OY 41 GlyLysAsnLeuSerGluAlaGlnLeuArGLeuLysLeuSerGluValaPheSerAspGly 60
Db 856 GGACAAACCAACCAAGAGAGAGATTCAGATATGATCAATGATGATGCTGATGAGC 915
OY 61 AspGlyGluLeuSerPheGlnGluPheLeuThr--AlaAlaArGlyLysAlaArG---- 77
Db 916 AATGAGACGATTTACTTCTGCTGATTTCTTACATGATGCTAGAAATAAGAGACACA 975
OY 78 AlaglyleugluaspLeugluValAlaPheArGAlaPheaspGlnaspGlyAspGlyHis 97
Db 976 GACAGCAGAGAGAAATCCGAGAGACATTCGCTGTTTGGACAGAGATGGAGAGGGCTAC 1035
OY 98 IlePheValaspGluLeuArGArGAlaMetAlaGlyLeuglyGlnProLeuProGlnGlu 117

Db 1036 ATCAGCCGCTGCTCAGTTACGTCACGTCATGACAAACCTCGGGGAGAGTTAACAGATGAA 1095
OY 118 GluLeuaspAlaMetIleArGAlaValaspAlaaspGlnaspGlyArGValaspGlyGlu 137
Db 1096 GAAGTTGATGAATAGTAAGAGAGAGATATCATGTGATGCGCAAGTAATATGAA 1155
OY 138 GluPheAlaArGMetLeu 143
Db 1156 GAGTTTGTACAAATGATG 1173

RESULT 10

US-08-100-874-1
; Sequence 1, Application US/08100874
; Patent No. 5498533
; GENERAL INFORMATION:
; APPLICANT: Pooviah, B. W.
; APPLICANT: Takezawa, D.
; APPLICANT: Han, T. J.
; APPLICANT: An, G. H.
; TITLE OF INVENTION: Control of Growth and Development of
; TITLE OF INVENTION: Potato Plants
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Harness, Dickey & Pierce
; STREET: P.O. Box 828
; CITY: Bloomfield Hills
; STATE: MI
; COUNTRY: USA
; ZIP: 48303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/100,874
; FILING DATE: July 30, 1993
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, Deann F.
; REFERENCE/DOCKET NUMBER: 7555-00004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (313) 641-1600
; TELEFAX: (313) 641-0270
; TELEX: 287637 Harness UR
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 906 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHEICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Solanum tuberosum
; INDIVIDUAL ISOLATE: P-PCM-1
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 81..530
US-08-100-874-1

Alignment Scores:
Pred. No.: 2.84e-35 Length: 906
Score: 355.50 Matches: 73
Percent Similarity: 69.868 Conservative: 29
Best Local Similarity: 50.008 Mismatches: 41
Query Match: 48.778 Indels: 3
DB: 1 Gaps: 2

US-10-031-403-1 (1-146) x US-08-100-874-1 (1-906)

OY 1 MetAlaGlyLeuLeuThrProGluGluGluAlaGlnTyrLysLysAlaPheSerAlaVal 20

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||||| ..... ||||| ..... ||||| ..... ||||| ..... ||||| .....
Db 81 ATGGCAGAGCAGCTGACGAGAGGAGCAGATGCCGAGTTCAAGAGACTTTAGCCTTTC 140
Oy 21 AspThrAspGlyAsnGlyThrIleAsnAlaGlnGluLeuGlyAlaAlaLeuLysAlaThr 40
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 141 GACAAAGATGGCGATGGCTGTATTAATACCAAGAGTTGGAAAGCTGATGATCATT 200
Oy 41 GlyLysAsnLeuSerGlnAlaGlnLeuArgLysLeuIleSerGlnValAlaSerAspGly 60
Db 201 GGTCAAGATCCCACTGAAGCTGACTACAGATATGATGAGTGAAGCTGATCTGATCAG 260
Oy 61 AspGlyGluIleSerPheGlnGluPheLeuThr---AlaAlaArgLysAlaArg----- 77
Db 261 AATGGACCATGATTTTCCAGAGTTCTTGAATCTGATGCGACGTAAGATGAAGACACT 320
Oy 78 AlaGlyLeuGluAspLeuGlnValAlaPheArgAlaPheAspGlnAspGlyAspGlyHis 97
Db 321 GATTCTGAGGAGCACTCAAGAGCTTTCAAGGTTTTCGATGAATGAGATGAAGACACT 380
Oy 98 IleThrValAspGluLeuArgArgAlaMetAlaGlyLeuGlyGlnProLeuProGlnGlu 117
Db 381 ATTCTGCGAGCTGAGCTTCTGATGTAATGACAAACCTTGGAGAGAGCTGACTGATGAA 440
Oy 118 GluLeuAspAlaMetIleArgGlnAlaAspValAspGlnAspGlyArgValAsnTyrglu 137
Db 441 GAGGTGATGATGATGATCGAGAGCAGCATATTGATGATGGCAGCACTTAATTATGAG 500
Oy 138 GluPheAlaArgMetLeu 143
Db 501 GAGTTTGTCCGTATGATG 518

RESULT 11
US-09-239-909-1
; Sequence 1, Application US/09239909
; Patent No. 6284952
; GENERAL INFORMATION:
; APPLICANT: Kumo Petrochemical Co. Ltd.
; TITLE OF INVENTION: Transgenic Plants with Divergent SCAM4 or SCAM5 Gene to Achieve
; FILE REFERENCE: P99-2-6
; CURRENT APPLICATION NUMBER: US/09/239,909
; EARLIER FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: EP 99300136.1
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: KOPATIN 1.0
; SEQ ID NO 1
; LENGTH: 1401
; TYPE: DNA
; ORGANISM: G. max calmodulin4 (SCAM4)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (657)..(1106)
US-09-239-909-1

Alignment Scores:
Pred. No.: 3,64e-31 Length: 1401
Score: 324.50 Matches: 65
Percent Similarity: 67.81% Conservative: 34
Best Local Similarity: 44.52% Mismatches: 44
Query Match: 44.51% Indels: 3
DB: 4 Gaps: 2

US-10-031-403-1 (1-146) x US-09-239-909-1 (1-1401)
Oy 1 MetalaglyGluLeuThrProGlnGluGlnAlaGlnIleTyrlsLysAlaPheSerAlaVal 20
Db 657 ATGGCAGATATCTCTGATGAGAGACAGATGTTGATTTTAAAGAGCCCTTGGCTTGT 716
Oy 21 AspThrAspGlyAsnGlyThrIleAsnAlaGlnGluLeuGlyAlaAlaLeuLysAlaThr 40
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 717 GACAAAGATGAGATGCTTGTACTGTGGAAGAACTGCCACAGTCTACTTGGCATTCG 776
Oy 41 GlyLysAsnLeuSerGlnAlaGlnLeuArgLysLeuIleSerGlnValAlaSerAspGly 60

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..... ||||| ..... ||||| ..... ||||| ..... ||||| ..... ||||| .....
Db 777 GATCAAGAACCCCACTGAAGAGAGCTCAAGATATGATTAAGCAAGTCAATGAGATGGC 836
Oy 61 AspGlyGluIleSerPheGlnGluPheLeuThr---AlaAlaArgLysAlaArg----- 77
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 837 AATGGACCATGATTAATGACGATTTGACCTTGATGAGCCCAAGAACTTAAGACACT 896
Oy 78 AlaGlyLeuGluAspLeuGlnValAlaPheArgAlaPheAspGlnAspGlyAspGlyHis 97
Db 897 GATCGAGAGGAGAGCTCAAGAGCTTTCAGGTTTGTGACAAAGATCAAAATGCTTAC 956
Oy 98 IleThrValAspGluLeuArgArgAlaMetAlaGlyLeuGlyGlnProLeuProGlnGlu 117
Db 957 ATATCAGCAGTAGAGTGTAGACACCAATGATGATCAATCTAAGGGGAAAAGTAAACCATGA 1016
Oy 118 GluLeuAspAlaMetIleArgGlnAlaAspValAspGlnAspGlyArgValAsnTyrglu 137
Db 1017 GAGGTGACAGATGATTTTAAAGAGCATTTTGACGATGATGCCCAAGTAACTATGAG 1076
Oy 138 GluPheAlaArgMetLeu 143
Db 1077 GAATTCGTCAAGATGATG 1094

RESULT 12
US-09-239-909-3
; Sequence 3, Application US/09239909
; Patent No. 6284952
; GENERAL INFORMATION:
; APPLICANT: Kumo Petrochemical Co. Ltd.
; TITLE OF INVENTION: Transgenic Plants with Divergent SCAM4 or SCAM5 Gene to Achieve
; FILE REFERENCE: P99-2-6
; CURRENT APPLICATION NUMBER: US/09/239,909
; EARLIER FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: EP 99300136.1
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: KOPATIN 1.0
; SEQ ID NO 3
; LENGTH: 916
; TYPE: DNA
; ORGANISM: G. max calmodulin5 (SCAM5)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (69)..(518)
US-09-239-909-3

Alignment Scores:
Pred. No.: 4,64e-29 Length: 916
Score: 305.50 Matches: 62
Percent Similarity: 63.70% Conservative: 31
Best Local Similarity: 42.47% Mismatches: 50
Query Match: 41.91% Indels: 3
DB: 4 Gaps: 1

US-10-031-403-1 (1-146) x US-09-239-909-3 (1-916)
Oy 1 MetalaglyGluLeuThrProGlnGluGlnAlaGlnIleTyrlsLysAlaPheSerAlaVal 20
Db 69 ATGGCAGATGTTCTGATGTAAGACAGATTAAGATGATCAAAAGAACCTTGTGCTTGT 128
Oy 21 AspThrAspGlyAsnGlyThrIleAsnAlaGlnGluLeuGlyAlaAlaLeuLysAlaThr 40
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 129 GACAAAGATGATGATGCTGATTAATGATGACGAAATTTGTCACGGTATCCGGTATG 188
Oy 41 GlyLysAsnLeuSerGlnAlaGlnLeuArgLysLeuIleSerGlnValAlaSerAspGly 60
Db 189 GTTCAGAACCCCACTGAAGAGAGCTCCAAAGCATGATTAAGAGAGATGATCCAGATGCT 248
Oy 61 AspGlyGluIleSerPheGlnGluPheLeuThrAlaAlaArgLysAlaArgAlaGlyLeu 80
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 249 AATGACACATGATTTTGTGATTTTGAATTAATGAGCCCAAGAAATGAAGAAACT 308
Oy 81 -----GluAspLeuGlnValAlaPheArgAlaPheAspGlnAspGlyAspGlyHis 97

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Db 309 GATCAGAGGAGATCTCAAGAGCTTCAAGGTGTTGACAGGACCAAAAGGCTAC 368
Qy 98 ILeThrValaSpLeuArgArgAlaMetAlaGlyLeuGlyGlnProLeuProGlnGlu 117
Db 369 ATTTCAGCAAGTGTGAGACAGCTTATGATCATCTGGGTGAAAACCTAACGATGAG 428
Qy 118 GluLeuAspAlaMetIleArgGlnAlaAspValaSpGlnAspGlyArgValaAsnTyrGlu 137
Db 429 GAGGTGGACGATGATGAAAGACAGATTGATGATGATGATGATGATGATGATGATGAT 488
Qy 138 GluPheAlaArgMetLeu 143
Db 489 GAATTGTCAGATGATG 506
RESULT 13
US-09-285-601-1
Sequence 1, Application US/09285601
Patent No. 6248528
GENERAL INFORMATION:
APPLICANT: Chen, Hong
APPLICANT: Frelmer, Nelson
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE DIAGNOSIS AND
FILE REFERENCE: 7853-089
CURRENT APPLICATION NUMBER: US/09/285, 601
EARLIER FILING DATE: 1999-04-02
EARLIER APPLICATION NUMBER: 60/080, 841
EARLIER FILING DATE: 1998-04-06
NUMBER OF SEQ ID NOS: 3
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
LENGTH: 1173
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (49)..(564)
US-09-285-601-1
Alignment Scores:
Pred. No.: 1,49e-26 Length: 1173
Score: 286.50 Matches: 62
Percent Similarity: 62.24% Conservative: 27
Best Local Similarity: 43.36% Mismatches: 51
Query Match: 39.30% Indels: 3
Gaps: 1
US-10-031-403-1 (1-146) x US-09-285-601-1 (1-1173)
Qy 4 GluLeuThrProGlnGluGlnAlaGlnTyrLysLysAlaPheSerAlaValaAspThrAsp 23
Db 118 GAGCTCACTGAGATCGAAGCAAGATTCGGGACCATTTGACCTTCGACGTGAC 177
Qy 24 GlyAsnGlyThrIleAsnAlaGlnGluGlnAlaValaLeuLysAlaThrGlyLysAsn 43
Db 178 GGAAGTGGACCATCGACCGGAAGAGCTGAGGCGCATGAGAGCGCTGGCTTGAA 237
Qy 44 LeuSerGlnAlaGlnLeuArgLysLeuIleSerGlnValaAspSerAspGlyAspGlyGlu 63
Db 238 CCCAGGAGGAGAGATGAGAAATGATCTCCGAGGTGACAGGAGGAGGAGGAGGAG 297
Qy 64 IleSerPheGlnGluPheLeu-----ThrAlaAlaArgLysAlaArgAlaGlyLeu 80
Db 298 ATGAGCTTCATGACTCTGGCGCGTGATGACGACAGAGATGTCCGAGAGGACACCAA 357
Qy 81 GluAspLeuGlnValaAlaPheArgAlaPheAspGlnAspGlyAsnIleThrVal 100
Db 358 GAAGAAATCTGGAAGGCTTCAGGCTTTGATGACATGACACCGGAGAAATCTGCTC 417
Qy 101 AspGluLeuArgArgAlaMetAlaGlyLeuGlyGlnProLeuProGlnGlnGluLeuAsp 120
Db 418 AAAAAGCTGAAGCGTGTGGCCAGAGCTGGGGAGAACTCAGCATGAGAGGCTGAC 477

Qy 121 AlaMetIleArgGlnAlaAspValaAspGlnAspGlyArgValaAsnTyrGlnGluPheAla 140
Db 478 GAGATGATCGACGAGACGATCGGATGGGACCGGAGAGTGAACGAGAGAGATTCCT 537
Qy 141 ArgMetLeu 143
Db 538 CGGATCATG 546
RESULT 14
US-09-285-601-3
Sequence 3, Application US/09285601
Patent No. 6248528
GENERAL INFORMATION:
APPLICANT: Chen, Hong
APPLICANT: Frelmer, Nelson
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE DIAGNOSIS AND
FILE REFERENCE: 7853-089
CURRENT APPLICATION NUMBER: US/09/285, 601
EARLIER FILING DATE: 1999-04-02
EARLIER APPLICATION NUMBER: 60/080, 841
EARLIER FILING DATE: 1998-04-06
NUMBER OF SEQ ID NOS: 3
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3
LENGTH: 6709
TYPE: DNA
ORGANISM: Homo sapiens
US-09-285-601-3
Alignment Scores:
Pred. No.: 1,62e-25 Length: 6709
Score: 286.50 Matches: 62
Percent Similarity: 62.24% Conservative: 27
Best Local Similarity: 43.36% Mismatches: 51
Query Match: 39.30% Indels: 3
Gaps: 1
US-10-031-403-1 (1-146) x US-09-285-601-3 (1-6709)
Qy 4 GluLeuThrProGlnGluGlnAlaGlnTyrLysLysAlaPheSerAlaValaAspThrAsp 23
Db 3015 GAGCTCACTGAGATCGAAGCAAGATTCGGGACCATTTGACCTTCGACGTGAC 3074
Qy 24 GlyAsnGlyThrIleAsnAlaGlnGluGlnAlaValaLeuLysAlaThrGlyLysAsn 43
Db 3075 GGAAGTGGACCATCGACCGGAAGAGCTGAGGCGCATGAGAGCGCTGGCTTGAA 3134
Qy 44 LeuSerGlnAlaGlnLeuArgLysLeuIleSerGlnValaAspSerAspGlyAspGlyGlu 63
Db 3135 CCCAGGAGGAGAGATGAGAAATGATCTCCGAGGTGACAGGAGGAGGAGGAGGAG 3194
Qy 64 IleSerPheGlnGluPheLeu-----ThrAlaAlaArgLysAlaArgAlaGlyLeu 80
Db 3195 ATGAGCTTCATGACTCTGCGCGTGATGACGACAGAGATGTCCGAGAGGACACCAA 3254
Qy 81 GluAspLeuGlnValaAlaPheArgAlaPheAspGlnAspGlyAsnIleThrVal 100
Db 3255 GAAGAAATCTGGAAGGCTTCAGGCTTTGATGACATGACACCGGAGAAATCTGCTC 3314
Qy 101 AspGluLeuArgArgAlaMetAlaGlyLeuGlyGlnProLeuProGlnGlnGluLeuAsp 120
Db 3315 AAAAAGCTGAAGCGTGTGGCCAGAGCTGGGGAGAACTCAGCATGAGAGGCTGAC 3374
Qy 121 AlaMetIleArgGlnAlaAspValaAspGlnAspGlyArgValaAsnTyrGlnGluPheAla 140
Db 3375 GAGATGATCGACGAGCTGATCGGATGGGACGAGAGTGAACGAGAGAGATTCCT 3434
Qy 141 ArgMetLeu 143
Db 3435 CGGATCATG 3443

GenCore version 5.1.4-p5.4578
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OM protein - nucleic search, using frame_plus_p2n model

Run on: May 16, 2003, 03:19:19 ; Search time 1748 Seconds

(without alignments)
1352.712 Million cell updates/sec

Title: US-10-031-403-1

Perfect score: 729

Sequence: 1 MAGELPDEEAQYKAFSAV.....DVDGDGRVNEEFARMLAE 146

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Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 16154066 segs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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-MODEL-frame+ p2n model -DEV-rlh
-O=/cgnr_1/USPRO.spool/US10031403/runat_08052003.131925_5691/app.query.fasta_1.327
-DB-EST -QFMT-fastlap -SUFFI-rst -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0
-UNITS-bits -STAR=1 -END=1 -MATRIX-Biosum62 -TRANS-human40.cdi -LIST=45
-DOCALLION=200 -THE_SCORE-pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT-pto -NORM-ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US10031403.cgnr_1.1.1906/runat_08052003.131925_5691 -NCPU=6 -ICPU=3
-NO_XLIPY -NO_MMAP -LARGESQUERY -NEG_SCORES=0 -WAIT -LONGLOC -DEV-TIMEOUT=120
-WAIT_TIMEOUT=30 -THRAPDS=1 -XGAPOP=10 -XGAPEXT=0.5 -Fgapop=6 -Fgapext=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :
1: EST:*
2: em_estba:*
3: em_estin:*
4: em_estinu:*
5: em_estlov:*
6: em_estlpl:*
7: em_estrio:*
8: em_htc:*
9: gb_estl1:*
10: gb_estl2:*
11: gb_htc:*
12: gb_estl3:*
13: gb_estl4:*
14: gb_estl5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vit:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rtd:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	726	99.6	721	12	BG696865
2	725	99.5	819	12	BG680086
3	725	99.5	867	12	BG697492
4	703	96.4	830	12	BG743203
5	699	95.9	976	12	BG676307
6	642	88.1	508	9	A1791325
7	642	88.1	508	9	A1791495
8	411	56.4	444	10	AM464722
9	398.5	54.7	537	10	BE012482
10	391.5	53.7	846	12	BF103910
11	390.5	53.6	499	9	AA770786
12	390.5	53.6	619	10	BE199943
13	389.5	53.4	603	12	BF297037
14	389.5	53.4	619	12	BF297132
15	389.5	53.4	746	13	BM160783
16	389.5	53.4	765	13	BM164242
17	389.5	53.4	781	13	BM164242
18	388.5	53.3	510	9	AA023153
19	388.5	53.3	517	13	BI936031
20	388.5	53.3	534	14	BM874967
21	388.5	53.3	596	10	AM765916
22	388.5	53.3	613	14	BQ633415
23	388.5	53.3	659	14	BM837142
24	388.5	53.3	808	9	AU079535
25	388.5	53.3	939	13	BM542199
26	387.5	53.2	646	13	BG974147
27	386.5	53.0	521	14	W10714
28	386.5	53.0	524	12	BE737663
29	386.5	53.0	573	14	BM839707
30	386.5	53.0	669	12	BG547553
31	386.5	53.0	718	12	BG705382
32	386.5	53.0	719	12	BG727110
33	386.5	53.0	755	12	BG699270
34	386.5	53.0	814	13	BI668543
35	386.5	53.0	816	12	BF666722
36	386.5	53.0	859	12	BG723324
37	386.5	53.0	869	12	BG703957
38	386.5	53.0	878	12	BF666960
39	386.5	53.0	883	12	BF696541
40	386.5	53.0	914	12	BG542960
41	385.5	52.9	565	10	AM537180
42	385.5	52.9	574	13	BI865062
43	385.5	52.9	627	12	BG507134
44	385.5	52.9	630	12	BG776331
45	385.5	52.9	712	10	AV715763

ALIGNMENTS

RESULT 1
LOCUS BG696865 721 bp mRNA linear EST 07-MAY-2001
DEFINITION 602658626F1 NCI_CGAP_Skn3 Homo sapiens CDNA clone IMAGE:4801854 5',
RNA sequence.
ACCESSION BG696865
VERSION BG696865.1 GI:13962457
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 721)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>..
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL COMMENT

Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgabs-remail.nih.gov
 Tissue Procurement: James Cleaver, M.D.
 CDNA Library Preparation: Life Technologies, Inc.
 Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Plate: LLAM10695 row: c column: 07
 High quality sequence stop: 697.
 Location/Qualifiers

FEATURES

source

1.721
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="IMAGE:4801854"
 /lab_host="NCI CGAP_Skn3"
 /note="Organ: Skin; Vector: PCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.5kb. Library constructed by Life Technologies. Note: this is a NCI CGAP Library."
 BASE COUNT 125 a 221 c 271 g 104 t
 ORIGIN

Alignment Scores:

Pred. No.: 5,66e-78 Length: 721
 Score: 726.00 Matches: 145
 Percent Similarity: 100.00% Conservative: 1
 Best Local Similarity: 99.32% Mismatches: 0
 Query Match: 99.59% Indels: 0
 Gaps: 0

US-10-031-403-1 (1-146) x BG696865 (1-721)

QY 1 MetAlAGlGluLeuThrProGluGluAlaGlnTyrLysAlaPheSerAlaVal 20
 Db 100 ATGGCCGCTGAGCTGCTCTGAGAGAGAGCCAGTACAAAGGCTTCTCCGCGGT 159
 QY 21 AspThrAspGlyAsnGlyThrIleAsnAlaGlnGluLeuGlyAlaAlaLeuLysAlaThr 40
 Db 160 GACACGATGGAAGGACACATCAATGCCAGAGCTGGCGCGCGCTGGAAGCCACG 219
 QY 41 GlyLysAsnLeuSerGluAlaGlnLeuArgLysLeuIleSerGluValAspSerAspGly 60
 Db 220 GGCAGAACCTCTCGAGGCCCGCAAGGAACTCATCTCCGAGGTTGACAGCGCGC 279
 QY 61 AspGlyGluIleSerPheGlnGluPheLeuThrAlaAlaArgLysAlaAlaGlyLeu 80
 Db 280 GACGGCGAAATCAGCTTCCAGAGTTCTTCAAGCGCGGCAAGAGCGCGGCGCTG 339
 QY 81 GluAspLeuGlnValAlaPheArgAlaPheAspGlnAspGlyHisIleThrVal 100
 Db 340 GAGGACCTGAGGTGCGCTTCCGCGCTTGCACAGATGGCAGCGCCATCACCGTG 399
 QY 101 AspGluLeuArgArgAlaMetAlaGlyLeuGlyGlnProLeuProGlnGluGluLeuAsp 120
 Db 400 GACGAGCTCAGCGCGGCAAGCGGCGCTGGCGAGCCGCTCCGAGAGAGAGCTGAC 459
 QY 121 AlaMetIleArgGluAlaAspValAspGlnAspGlyArgValAsnTyrGluGluPheAla 140
 Db 460 GCCATGATCCGAGCGCGCTGACACAGAGCGGCGGTGAATCAGAGGAGTTGCGG 519
 QY 141 ArgMetLeuAlaGlnGlu 146
 Db 520 AGGATGCTGCCAGAGAG 537
 RESULT 2
 LOCUS BG680086 819 bp mRNA linear EST 01-MAY-2001
 DEFINITION 602682828F1 NCI_CGAP_Skn4 Homo sapiens cDNA clone IMAGE:4753280 5',
 mRNA sequence.

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

BG680086
 BG680086.1 GI:13911483
 EST.
 human.
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE AUTORS TITLE JOURNAL COMMENT

NIH-MGC <http://imgc.nci.nih.gov/>
 1 (bases 1 to 819)
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgabs-remail.nih.gov
 Tissue Procurement: James Cleaver, M.D.
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Plate: LLAM10612 row: k column: 09
 High quality sequence stop: 819.
 Location/Qualifiers

FEATURES

source

1.819
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="IMAGE:4753280"
 /clone_lib="NCI CGAP_Skn4"
 /tissue_type="squamous cell carcinoma"
 /lab_host="DH10B (T1 phage-resistant)"
 /note="Organ: Skin; Vector: PCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.5kb. Library constructed by Life Technologies. Note: this is a NCI CGAP Library."
 BASE COUNT 139 a 256 c 300 g 124 t
 ORIGIN

Alignment Scores:

Pred. No.: 9e-78 Length: 819
 Score: 725.00 Matches: 145
 Percent Similarity: 99.32% Conservative: 0
 Best Local Similarity: 99.32% Mismatches: 1
 Query Match: 99.45% Indels: 0
 Gaps: 0

US-10-031-403-1 (1-146) x BG680086 (1-819)

QY 1 MetAlAGlGluLeuThrProGluGluAlaGlnTyrLysAlaPheSerAlaVal 20
 Db 117 ATGGCCGCTGAGCTGCTCTGAGAGAGAGCCAGTACAAAGGCTTCTCCGCGGT 176
 QY 21 AspThrAspGlyAsnGlyThrIleAsnAlaGlnGluLeuGlyAlaAlaLeuLysAlaThr 40
 Db 177 GACACGATGGAAGGACACATCAATGCCAGAGCTGGCGCGCGCTGGAAGCCACG 236
 QY 41 GlyLysAsnLeuSerGluAlaGlnLeuArgLysLeuIleSerGluValAspSerAspGly 60
 Db 177 GACACGATGGAAGGACACATCAATGCCAGAGCTGGCGCGCGCTGGAAGCCACG 236
 QY 61 AspGlyGluIleSerPheGlnGluPheLeuThrAlaAlaArgLysAlaAlaGlyLeu 80
 Db 237 GGCAGAACCTCTCGAGGCCCGCAAGGAACTCATCTCCGAGGTTGACGCGGAGCGC 296
 QY 81 GluAspLeuGlnValAlaPheArgAlaPheAspGlnAspGlyHisIleThrVal 100
 Db 297 GACGGCGAAATCAGCTTCCAGAGTTCTTCAAGCGCGGCAAGAGCGCGGCGCTG 356
 QY 101 AspGluLeuArgArgAlaMetAlaGlyLeuGlyGlnProLeuProGlnGluGluLeuAsp 120
 Db 357 GAGGACCTGAGGTGCGCTTCCGCGCTTGCACAGATGGCAGCGCCATCACCGTG 416
 QY 101 AspGluLeuArgArgAlaMetAlaGlyLeuGlyGlnProLeuProGlnGluGluLeuAsp 120
 Db 417 GACGAGCTCAGCGCGGCAAGCGGCGCTGGCGAGCCGCTCCGAGAGAGAGCTGAC 476
 QY 121 AlaMetIleArgGluAlaAspValAspGlnAspGlyArgValAsnTyrGluGluPheAla 140
 Db 121 AlaMetIleArgGluAlaAspValAspGlnAspGlyArgValAsnTyrGluGluPheAla 140

Db 477 GCCATGATCCGAGCGCCAGCTGACGACGAGCGCGGTGACTACGAGAGTTCCGC 536
 Oy 141 ArgmetleuaglInglu 146
 Db 537 AGGATGCTGCCAGAG 554
 RESULT 3
 BG697492
 LOCUS 867 bp mRNA linear EST 07-MAY-2001
 DEFINITION 602660685F1 NCI_CGAP_Skn3 Homo sapiens cDNA clone IMAGE:4803932 5',
 mRNA sequence.
 ACCESSION BG697492
 VERSION BG697492.1 GI:13963770
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 REFERENCE 1 (bases 1 to 867)
 NIH-MGC http://mgi.nci.nih.gov/.
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: James Cleaver, M.D.
 CDNA Library Preparation: Life Technologies, Inc.
 Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLM10700 row: 1 column: 21
 High quality sequence stop: 828.
 Location/Qualifiers
 1..867
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_image="4803932"
 /clone_lib="NCI_CGAP_Skn3"
 /lab_host="DH10B (T1 phage-resistant)"
 /note="Organ: Skin; Vector: pCMV-SPORT6; Site_1: NotI;
 Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
 Average insert size 1.5kb. Library constructed by Life
 Technologies. Note: this is a NCI_CGAP Library."
 BASE COUNT 187 a 252 c 296 g 132 t
 ORIGIN
 Alignment Scores:
 Pred. No.: 9.77e-78 Length: 867
 Score: 725.00 Matches: 145
 Percent Similarity: 99.32% Conservative: 0
 Best Local Similarity: 99.32% Mismatches: 1
 Query Match: 99.45% Indels: 0
 Gaps: 0
 US-10-031-403-1 (1-146) x BG697492 (1-867)
 Oy 1 MetAlaGlyLeuThrProGluGluAlaGlnTyrTyrLysAlaPheSerAlaVal 20
 Db 78 ATGGCCGGTGAAGCTCTCTGAGAGAGAGCCAGTACAAAAGGCTTCTCCGGGTT 137
 Oy 21 AspThrAspGlyAsnGlyThrIleAsnAlaGlnGluLeuGlyAlaAlaLeuLysAlaThr 40
 Db 138 GACACGAGATGGAACGGACCATCAATGCGCCAGAGAGCTGGCGGCGCTGAAGGCACG 197
 Oy 41 GlyLysAsnLeuSerGluAlaGlnLeuArgLysLeuIleSerGluValAspSerAspGly 60
 Db 198 GGCAAGAACCTCTCTCGAGAGCCAGCTAAGGAAATCATCTCCGAGCTGACGCGCAGC 257
 Oy 61 AspGlyLysIleSerPheGlnGluPheLeuThrAlaAlaArgLysAlaArgAlaGlyLeu 80
 Db 258 GACGCGAAATATCAGCTTCCAGAGATTCTTGACGCGGCGCAAGAGGCCAGGCGGCTTG 317

Oy 81 GluAspLeuGlnValAlaPheArgAlaPheAspGlnAspGlyAspGlyHisIleThrVal 100
 Db 318 GAGGACCTCAGAGTCCCTCCGCGCTTGCACAGAGATGGGAGCGCCACATCACCGTG 377
 Oy 101 AspGluLeuArgAlaMetAlaGlnGlyGlnProLeuProGlnGluLeuAsp 120
 Db 378 GACGAGCTCAGCGCGGCCATGCGCGGCGGCGACCCCTCCGACGAGAGAGCTGAGC 437
 Oy 121 AlaMetIleArgGluAlaAspValAspGlyArgValAspThrGlnGluPheAla 140
 Db 438 GCCATGATCCGAGAGCCGAGCTGACGACGAGGCGGGGTGAATCAAGAGAGATTCCGC 497
 Oy 141 ArgMetLeuaglInglu 146
 Db 498 AGGATGCTGCCAGAG 515
 RESULT 4
 BG743203
 LOCUS 830 bp mRNA linear EST 15-MAY-2001
 DEFINITION 602634365F1 NCI_CGAP_Skn3 Homo sapiens cDNA clone IMAGE:4779184 5',
 mRNA sequence.
 ACCESSION BG743203
 VERSION BG743203.1 GI:14053856
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 REFERENCE 1 (bases 1 to 830)
 NIH-MGC http://mgi.nci.nih.gov/.
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: James Cleaver, M.D.
 CDNA Library Preparation: Life Technologies, Inc.
 Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLM10636 row: b column: 17
 High quality sequence stop: 823.
 Location/Qualifiers
 1..830
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_image="4779184"
 /clone_lib="NCI_CGAP_Skn3"
 /lab_host="DH10B (T1 phage-resistant)"
 /note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI;
 Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
 Average insert size 1.5kb. Library constructed by Life
 Technologies. Note: this is a NCI_CGAP Library."
 BASE COUNT 139 a 257 c 303 g 131 t
 ORIGIN
 Alignment Scores:
 Pred. No.: 4.31e-75 Length: 830
 Score: 703.00 Matches: 144
 Percent Similarity: 97.96% Conservative: 0
 Best Local Similarity: 97.96% Mismatches: 2
 Query Match: 96.43% Indels: 1
 Gaps: 0
 US-10-031-403-1 (1-146) x BG743203 (1-830)
 Oy 1 MetAlaGlyLeuThrProGluGluAlaGlnTyrTyrLysAlaPheSerAlaVal 20
 Db 121 ATGGCCGGTGAAGCTCTCTGAGAGAGAGCCAGTACAAAAGGCTTCTCCGGGTT 180
 Oy 21 AspThrAspGlyAsnGlyThrIleAsnAlaGlnGluLeuGlyAlaAlaLeuLysAlaThr 40

```

Db 181 GACACGATGGAAGGACCATCATGCTCCAGAGCTGTCGCCGCGCTGAAGCCAC 240
Qy 40 rgltyAsnleuSerGluaInleuArglySleuIleSerGluaValAspSerasp1 60
Db 241 GGGCAAGAACCTCTCGAGAGCCAGCTAAGAAACATCATCTCGAGGTGAGCGGCG 300
Qy 60 yAspGlyIuIleSerPheGlnGluPheLeuThrAlaAlaArglySAlaArgAlaGlyLe 80
Db 301 CGAGCGGGAATCAGCTTCAGAGAGTTCCTGACGCGCGCAAGAGGCCAGCGCGCT 360
Qy 80 uGluAspLeuGlnValAlaPheArgAlaPheAspGlnAspGlyAspGlyHisIleThrVa 100
Db 361 GAGAGGACCTCAGGTCCTTCGCGCTTCGACAGAGATGGCGCGCCACATCACCCT 420
Qy 100 lAspGluLeuArgAlaMetAlaGlyLeuGlyGlnProLeuProGlnGluLeuAs 120
Db 421 GGACGAGCTCAGCGCGGCGCTGCGGGGCGACCGCTCGCGGAGAGAGCTGGA 480
Qy 120 pAlaMetIleArgGluAlaAspValAspGlnAspGlyArgValAsnTyrGluGluPheAl 140
Db 481 CGCAGATGATCCGGAGCGCCAGCTGACGAGAGCGGGGTGAATCAAGAGAGTTCGC 540
Qy 140 aArgMetLeuAlaGlnGlu 146
Db -541 GAGATGCTCGCCAGAG 559

RESULT 5
Bg676307 976 bp mRNA linear EST 01-MAY-2001
LOCUS 60262271.F1 NCI_CGAP_Skn4 Homo sapiens cDNA clone IMAGE:4747661 5',
DEFINITION mRNA sequence.
ACCESSION Bg676307
VERSION Bg676307.1 GI:13907703
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 976)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: James Cleaver, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLNL0598 row: a column: 06
High quality sequence stop: 820.
Location/Qualifiers
1. 976
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4747661"
/tissue="NCI_CGAP_Skn4"
/lab_host="DH10B (T1 phage-resistant)"
/notes="Organ: skin; Vector: pCMV-SPORT6; Site:1: NotI;
Site:2: SalI; Cloned unidirectionally.
Average insert size 1.5kb. Library constructed by Life
Technologies. Note: this is a NCI_CGAP Library."

BASE COUNT 234 a 263 c 342 g 137 t
ORIGIN
Alignment Scores:
Pred. No.: 1.66e-74 Length: 976
Score: 699.00 Matches: 144
Percent Similarity: 99.32% Conservative: 1
Best Local Similarity: 98.63% Mismatches: 1

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Query Match: 95.88% Indels: 1
DB: 12 Gaps: 0
US-10-031-403-1 (1-146) x Bg676307 (1-976)

Qy 1 MetAlaGlyIuLeuThrProGlnGluGluAlaGlnTyrIleSylsAlaPheSerAlaVal 20
Db 115 ATGGCCGGTGAAGCTCTGAGAGAGAGGCCAGTACAAAGAGGCTTCTCGCGCTT 174
Qy 21 AspThrAspGlyAsnGlyThrIleAsnAlaGlnGluLeuGlyAlaAlaLeuLyAlaThr 40
Db 175 GACACGATGGAAGGACCATCATGCTCCAGAGAGCTGGGCGCGGCTGAAGGCCACG 234
Qy 41 GLyAsnleuSerGluaInleuArglySleuIleSerGluaValAspSerasp1 60
Db 235 GGCAGAAACCTCTCGAGAGCCACACTAAGAACTCATCTCGAGGTGACAGCGAGCC 294
Qy 61 AspGlyIuIleSerPheGlnGluPheLeuThrAlaAlaArglySAlaArgAlaGlyLeu 80
Db 295 GAGCGGAAATCAGCTTCAGAGAGTTCCTGACGCGCGCAAGAGGCCAGGCC-GGCCTG 353
Qy 81 GluAspLeuGlnValAlaPheArgAlaPheAspGlnAspGlyAspGlyHisIleThrVal 100
Db 354 GAGGACCTGCAAGTCGCTTCGCGCTTCGACAGAGATGGCGCGCCACATCACCCTG 413
Qy 101 AspGluLeuArgAlaMetAlaGlyLeuGlyGlnProLeuProGlnGluLeuAsp 120
Db 414 GACAGCTCAGCGCGGCGCATAGCGGCGCTGCGCGCGAGAGAGACTGGAC 473
Qy 121 AlMetIleArgGluAlaAspValAspGlnAspGlyArgValAsnTyrGluGluPheAla 140
Db 474 GCCATGATCCGCGAGCGCGAGGTGACAGAGAGCGGGGTGAATCAAGAGAGTTCGCG 533
Qy 141 ArgMetLeuAlaGlnGlu 146
Db 534 AGATGCTCGCCAGAG 551

RESULT 6
Al791325 508 bp mRNA linear EST 24-OCT-2000
LOCUS ae56g09.y5 StrataGene lung carcinoma 937218 Homo sapiens cDNA clone
DEFINITION IMAGE:950944 5' similar to SW:CALM_PLAFA P24044 CALMODULIN.; mRNA
sequence.
ACCESSION Al791325
VERSION Al791325.1 GI:5339041
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 508)
NCI-CGAP http://www.nci.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
other_ESTS: ae56g09.y5
Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
This read is a RESEQUENCE of a previously sequenced human clone
Original clone citation: see original entry for original citation
information
This 5' resequenced clone has no previous 5' data to verify this
new read against
Insert Length: 587 Std Error: 0.00
Seq primer: -40RP from Glibco
High quality sequence stop: 486.
Location/Qualifiers
1. 508
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:950944"

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/clone_lib="Stratagene lung carcinoma 937218"
/tissue_type="lung carcinoma"
/cell_line="NCI-H69"
/dev_stage="cell line NCI-H69"
/lab_host="SOLR (kanamycin resistant)"
/notes="Organ: lung; Vector: pBluescript SK-; Site: 1: EcoRI
; Site 2: XhoI; Cloned unidirectionally. Primer: Oligo
dt. Small cell carcinoma cell line NCI-H69. Average
insert size: 1.0 kb; Uni-ZAP XR Vector: -5' adaptor
sequence: 5' GATTTCGGCAGAG 3' -3' adaptor sequence: 5'
CTCAGCTTTTCTTTTCTTTTCTTTT 3'"
BASE COUNT 100 a 153 c 189 g 65 t 1 others
ORIGIN
Alignment Scores:
Pred. No.: 5,42e-68 Length: 508
Score: 642.00 Matches: 129
Percent Similarity: 98.47% Conservative: 0
Best Local Similarity: 98.47% Mismatches: 2
Query Match: 98.07% Indels: 0
DB: 9 Gaps: 0
US-10-031-403-1 (1-146) x A1791325 (1-508)
QY 1 MetalaGlyGluLeuThrProGluGluAlaGlnTyrLysAlaPheSerAlaVal 20
DB 115 ATGCCCGGTGAGCTGACCTCTGAGAGAGAGGCCCAAGAAAGCTTCTCCCGGTT 174
QY 21 AsptHraSpGlyAsnGlyThrIleAsnAlaGlnGluLeuGlyAlaIleLeuysAlaThr 40
DB 175 GACAGGATGAGAAAGGACCATCAATGCCAGAGAGCGGCGCTGAAAGCCACAG 234
QY 41 GlyLysAsnLeuSerGluAlaGlnLeuArgLysLeuIleSerGluValAspSerAspGly 60
DB 235 GGCAAGAACCTCTCGAGAGCCCAAGAAACTATCTCCGAGTTTACGCGACGCG 294
QY 61 AspGlyGluIleSerPheGlnGluPheLeuThrAlaAlaArgLysAlaArgAlaGlyLeu 80
DB 295 GACGGCGAATCAGCTTCAGAGAGTTCGAGCGGCGCAAGAAAGGCGCGCGCTG 354
QY 81 GluAspLeuGlnValAlaPheArgAlaPheAspGlnAspGlyAspGlyHisIleThrVal 100
DB 355 GAGGACCTGACAGTCCCTCCGCGCTTCGACAGAGAGCGGCGCCATCACCCGTG 414
QY 101 AspGluLeuArgArgAlaMetAlaGlyLeuGlnProLeuProGlnGluLeuAsp 120
DB 415 GACGAGCTCAGCGCGGCCCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 474
QY 121 AlaMetIleArgGluAlaAspValAspGlnAsp 131
DB 475 GCCATGATCCGCGAGCGGCGAGCTGACGACGAC 507
RESULT 7
A1791495 508 bp mRNA linear EST 13-DEC-1999
LOCUS n101f09.y5 NCI CGAP Br2 Homo sapiens cDNA IMAGE:966761 5'
DEFINITION similar to SW:CALM_PLAFA P24044 CALMODULIN.; mRNA sequence.
ACCESSION A1791495
VERSION A1791495.1 GI:5339211
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 508)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLES National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
JOURNAL Other ESTs: n101f09.s1
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nlm.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

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Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/BLINL at:
www.bio.lnlnl.gov/dbtrp/image/image.html
This read is a RESEQUENCE of a previously sequenced human clone
Original clone citation: see original entry for original citation
Information
This 5' resequenced clone has no previous 5' data to verify this
new read against
Insert Length: 336 Std Error: 0.00
Seq primer: -40RP from Gibco
High quality sequence stop: 464.
FEATURES
source
1..508
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_image="966761"
/clonelib="NCI-CGAP_Br2"
/sex="female, pooled"
/tissue_type="breast"
/lab_host="DH10B"
/notes="Vector: p773D-Pac (Pharmacia) with a modified
polylinker: 1st strand cDNA was prepared from pooled bulk
breast tumor tissue, and was then primed with a Not I -
oligo(dt) primer. Double-stranded cDNA was ligated to Eco
RI adaptors (Pharmacia), digested with Not I and cloned
into the Not I and Eco RI sites of the modified p773
vector. This library is the normalized version of
NCI CGAP Br1.1. Library was constructed by Bento Soares
and M. Fatima Bonaldo."
BASE COUNT 100 a 154 c 189 g 64 t 1 others
ORIGIN
Alignment Scores:
Pred. No.: 5,42e-68 Length: 508
Score: 642.00 Matches: 129
Percent Similarity: 98.47% Conservative: 0
Best Local Similarity: 98.47% Mismatches: 2
Query Match: 98.07% Indels: 0
DB: 9 Gaps: 0
US-10-031-403-1 (1-146) x A1791495 (1-508)
QY 1 MetalaGlyGluLeuThrProGluGluAlaGlnTyrLysAlaPheSerAlaVal 20
DB 115 ATGCCCGGTGAGCTGACCTCTGAGAGAGAGGCCCAAGAAAGCTTCTCCCGGTT 174
QY 21 AsptHraSpGlyAsnGlyThrIleAsnAlaGlnGluLeuGlyAlaIleLeuysAlaThr 40
DB 175 GACAGGATGAGAAAGGACCATCAATGCCAGAGAGCGGCGCTGAAAGCCACAG 234
QY 41 GlyLysAsnLeuSerGluAlaGlnLeuArgLysLeuIleSerGluValAspSerAspGly 60
DB 235 GGCAAGAACCTCTCGAGAGCCCAAGAAACTATCTCCGAGTTTACGCGACGCG 294
QY 61 AspGlyGluIleSerPheGlnGluPheLeuThrAlaAlaArgLysAlaArgAlaGlyLeu 80
DB 295 GACGGCGAATCAGCTTCAGAGAGTTCGAGCGGCGCAAGAAAGGCGCGCGCTG 354
QY 81 GluAspLeuGlnValAlaPheArgAlaPheAspGlnAspGlyAspGlyHisIleThrVal 100
DB 355 GAGGACCTGACAGTCCCTCCGCGCTTCGACAGAGAGCGGCGCCATCACCCGTG 414
QY 101 AspGluLeuArgArgAlaMetAlaGlyLeuGlnProLeuProGlnGluLeuAsp 120
DB 415 GACGAGCTCAGCGCGGCCCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 474
QY 121 AlaMetIleArgGluAlaAspValAspGlnAsp 131

```


BASE COUNT	236 a	147 c	233 g	230 t
ORIGIN	Library."			
Alignment Scores:	Lab-type="embryonal carcinoma"			
Pred. NO.:	/lab_host-DH10B (11 phage-resistant)			
Score:	2.96e-37	/note="Organ: testis; Vector: pDNR-LIB (Clontech); Site:1:		
Percent Similarity:	391.50	Sfil (ggccctcgcgcgc); Site-2: Sfil (ggccatctggcc);		
Percent Local Similarity:	74.66%	Double-stranded cDNA was prepared from cell line RNA. 5'		
Query Match:	52.74%	and 3' adaptors were used in cloning as follows: 5'		
	53.70%	adaptor sequence: 5'-ATCTGTAGAGCCGACGGCGGCACATC-dt(30)BN-3'		
	12	sequence: 5'-ATCTGTAGAGCCGACGGCGGCACATC-dt(30)BN-3'		
		(where B = A, C, G or G and N = A, C, G, or T). Average		
		insert size 1.75 kb (range 0.9-4.0 kb). 15/15 colonies		
		contained inserts by PCR. This library was enriched for		
		full-length clones and was constructed by Clontech		
		Laboratories (Palo Alto, CA). Note: this is a NIH-MGC		
		Library."		
US-10-031-403-1 (1-146) x BFI03910 (1-846)				
OY	1	MetAlaGlyGluLeuThrProGluGluGluAlaGlnTyrLysAlaPheSerAlaVal	20	
Db	50	ATGCGTGGCCCACTACTACGAGACAGCAGATTCGACAAATTCMAAGAAGCTTTTCACTATT	109	
OY	21	AspThrAspGlyAsnGlyThrIleAsnAlaGlnGluLeuGlyAlaAlaLeuLysAlaThr	40	
Db	110	GACAAAGATGGTGATGAGTAATACACAAAGAAATGGGAATGTAATGATGATCTT	169	
OY	41	GlyLysAsnLeuSerGluAlaGlnLeuArgLysLeuIleSerGluValAspSerAspGly	60	
Db	170	GGCGAGATCCACAGCAGAGAGAGTTACAGGACATGATTAAGAATGATGATCTATGCT	229	
OY	61	AspGlyGluIleSerPheGlnGluPheLeuThr-----AlaAlaArgLysAlaArg-----	77	
Db	230	AATGGCCACAAATTTGACTTCCCTCGAATTTCTGACAAATGATGGCAGAAATAATGAACACACA	289	
OY	78	AlaGlyLeuGluAspLeuGlnValAlaPheArgAlaPheAspGlnAspGlyAspLys	97	
Db	290	GACAGTGAAGAAGAATTAAGAAAGCATTCGCTGCTTTGATTAAGGATGGCAATGGCTAT	349	
OY	98	IleThrValAspGluLeuArgAlaGlnAlaGlyLeuGlyGlnProLeuProGlnGlu	117	
Db	350	ATTAGTGTCTGCAGAACTTCGCCATGTGATGACAAACCTTGGAGAACGTTAACACATGAA	409	
OY	118	GluLeuAspAlaMetIleArgGluAlaAspValAspGlnAspGlyArgValAspTyrGlu	137	
Db	410	GAAATTTGATGAAGAATGATGAGGAGAACATATTTGATGTTGATGATGATCAAGTAACATGAA	469	
OY	138	GluPheAlaArgMetLeu	143	
Db	470	GAGTTTGTACAAATGATG	487	
RESULT 11				
LOCUS	AA770786	499 bp	mRNA	linear
DEFINITION	vcl2a05.r1 Barstead mouse myoblasts MRLB5 Mus musculus cDNA clone			
ACCESSION	AA770786	IMAGE1162832 5' similar to gb:J04046 CALMODULIN (HUMAN); gb:x614322		
VERSION	AA770786.1	GI:2822597		
KEYWORDS	M.musculus mRNA for calmodulin (MOUSE); mRNA sequence.			
SOURCE	house mouse.			
ORGANISM	Mus musculus			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			

BASE COUNT	246 a	68 c	115 g	173 t	1 others
ORIGIN					
Alignment Scores:					
Pred. No.:	3.18e-37	Length:	603		
Score:	389.50	Matches:	76		
Percent Similarity:	73.97%	Conservative:	32		
Best Local Similarity:	53.05%	Mismatches:	35		
Query Match:	53.43%	Indels:	3		
DB:	12	Gaps:	2		
US-10-031-403-1 (1-146) x BF297037 (1-603)					
QY	1	METALAGYGLULeuThProgluGLUGLUALAGINTYRLYSALaPheSerAlaVal	20		
DB	49	ATGGCAGACAACTTACACAGAACAAATTCTGATTCGAAGACCTTCGTTGTT	108		
QY	21	ASpThrASpGlyASnGlyThrTlleASnAlaGInGLULeuGlyAlaAlaLeuLysAlaThr	40		
DB	109	GATTAAGAGATGCGAGATGGAACCACTAACCAACAAAGAACTAGCTGTCATGCGATCGTTG	168		
QY	41	GLYLSASnLeuSerGlnAlaGInLeuArgLysLysLleSerGlnLValASpSerASpGly	60		
DB	169	GGACAAACCCCAACGCAAGCAGACTACAGATGATTAATGAATTGACCAATGGG	228		
QY	61	ASpGlyGLULeuSerPheGInGLULeuThr---AlaAlaArgLysAlaArg-----	77		
DB	229	AATGATCAATGATGATTTCCCAAGATTTTAACTTTAATGGCAAGAAATGAAGATACA	288		
QY	78	AlaGlyLeuGInLAspLeuGInLValAlaPheArgAlaPheASpGlnASpGlyASpLys	97		
DB	289	GATPACGAAGAAGAAATTAATTGACCACTTTAAGATTTTGTATGAGATGCTATGCAAT	348		
QY	98	ILeThrValASpGLeuLeuArgArgAlaMeTAlaGlyLeuGlyGlnProLeuProGInGLU	117		
DB	349	ATCAGTGCCTGATGATTAAGACAGCTTATGACAAACCTAGGGGAAAACTCAAAATGA	408		
QY	118	GLULeuASpAlaMeTleArgGLUALaASpValASpGlnASpGlyArgValASnTYrGLU	137		
DB	409	GAGTTGATGAATGATGATTAAGACAGCTGACATAGATGAGATGGACAAATTAATATGAG	468		
QY	138	GLUPhaAlaArgMetLeu	143		
DB	469	GAGTTTGTTAATAATGATG	486		
RESULT 14					
LOCUS	BF297132				
DEFINITION	047DbF01 Pb cDNA #17, Tommaso Pace, Maria Ponzil, and Clara Frontalini	619 bp	mRNA	linear	EST 04-MAY-2001
ACCESSION	BF287132				
VERSION	BF297132.1				
KEYWORDS	EST.				
SOURCE	Plasmodium berghei.				
ORGANISM	Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.				
REFERENCE	1 (bases 1 to 619)				
AUTHORS	Carlton, J.M.-R. and Dame, J.B.				
TITLE	The Plasmodium vivax and P. berghei gene sequence tag projects				
JOURNAL	Parasitol. Today (Regul. Ed.) 16 (10), 409 (2000).				
COMMENT	Contact: Dame JB Department of Pathobiology, College of Veterinary Medicine University of Florida 2015 SW 23rd Avenue, Bldg 1017, Gainesville, FL 32611-0880, USA Tel: 352 392 4700 Fax: 352 392 9704				

Email: damej@mail.vetmed.wfl.edu
Seq primer: T3.

FEATURES

Location/Qualifiers
1. 619

/organism="Plasmodium berghiei"
/strain="ANKA clone HP (gametocyte producer)"

/db_xref="taxon:5821"
/clone_lib="Pd CDNA #17, Tommaso Pace, Marta Ponzi, and Clara Frontali"

/dev_stage="asynchronous blood stage"
/lab_host="Wistar rats"

/note="Vector: pBluescript II vector DNA, excised from Lambda ZAP II.; Site 1: EcoRI; Site 2: XhoI; Total RNA was extracted from asynchronous blood stage forms of the cloned ANKA isolate of P. berghiei, grown in Wistar rats to 30% parasitemia and 2-5% gametocytemia. Contaminating host white cells had previously been removed and final host cell contamination estimated to be approximately 5%.

PolyA+ RNA was extracted and reverse transcribed using an oligo dT-XhoI primer (lambda ZAP II cDNA cloning kit, Stratagene). Second strand cDNA was made following the manufacturer's protocol. EcoRI adaptors were ligated to the cDNA, and fragments were ligated into EcoRI/XhoI digested vector."

BASE COUNT 253 a 68 c 115 g 183 t.

ORIGIN

Alignment Scores:

Pred. No.: 3.3e-37 Length: 619
Score: 389.50 Matches: 76
Percent Similarity: 73.97% Conservative: 32
Best Local Similarity: 52.05% Mismatches: 35
Query Match: 53.43% Indels: 2
Gaps: 2

US-10-031-403-1 (1-146) x BF297132 (1-619)

QY 1 MetlaaglyleuthrProglugluAlaInTyrlsYlsAlaPheSerAlaVal 20

Db 49 ATGCAGACAGAGTTAAAGCAAGCAATTTCTGAATTCAGAAAGACGTTTCAGTTT 108

QY 21 AsphraspglyasnnglyThrIleasnlaaglInuaglyAlaIleuLysAlaThr 40

Db 109 GATTAAGATGAGATGAGACCATTAACAACAAGAAAGAGTACTGTCATCGATCGTTG 168

QY 41 GlyLysasnLeuSerGluAlaGlnLeuArgLysLeuSerGluValAspSerAspGly 60

Db 169 GGACAAACCAACGAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 228

QY 61 AspglyleuLysSerPheGlnGlnPheLeuThr---AlaAlaArgLysAlaArg---- 77

Db 229 AATGATCAATGATTTCCCGCAATTTTAACTTAAATGCAAAAGAAATGAAAGATACA 288

QY 78 AlaaglyleuGluAspGlnValAlaPheArgAlaPheAspGlnAspGlyAspGlyHis 97

Db 289 GATCAGACAGAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 348

QY 98 IleThrValAspglyleuArgArgAlaMetAlaGlyleuGlyGlnProLeuProGlnGlu 117

Db 349 ATCAGTGTGATGAATTAAGACAGCTTATGACAAACCTAGAGGAAACCAACCAATGA 408

QY 118 GluLeuAspAlaMetIleArgGluAlaAspValAspGlnAspGlyArgValAspGlyGlu 137

Db 409 GAACTTATGAATGAATGAATGAATGAATGAATGAATGAATGAATGAATGAATGAAT 468

QY 138 GluPheAlaArgMetLeu 143

Db 469 GAGTTTGTAAATGATG 486

RESULT 15

LOCUS BM160783 746 bp mRNA linear EST 04-DEC-2001
DEFINITION EST563306 PYBS Plasmodium yoelii yoelii cDNA clone PYCJ90 5' end.

FEATURES

Accession
BM160783
Version
BM160783.1 GI:17306464

KeyWords
EST.
Source
Plasmodium yoelii yoelii.

Organism
Plasmodium yoelii yoelii.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.

Reference
Carlton, J.M., Daly, J.M., Long, C.A., Bergman, L.W., Valdivia, A.B., Fraser, C.M., and Carucci, D.J. Plasmodium yoelii EST project at TIGR (bases 1 to 746)

Authors
Fraser, C.M., and Carucci, D.J.

Title
Unpublished (2001)

Journal
Contact: Jane Carlton

Comment
Parasite Genomics Group
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-530-9319
Fax: 301-838-0208

Email: carlton@tigr.org

For clone info, please contact the Malaria Research and Reference Reagent Resource Center, ATCC

http://www.malaria.mrl.org/m4pages/index.html

Seq primer: ADF.

FEATURES

Location/Qualifiers
1. 746

/organism="Plasmodium yoelii yoelii"
/strain="17XL"

/db_xref="taxon:73239"
/clone="PYCJ90"

/clone_lib="PYBS"
/dev_stage="asexual blood stages"

/lab_host="E. coli XL-1 Blue"

/note="Vector: PAD-GAL4; At 20-25% parasitemia, blood was collected from BALB/cBYJ mice infected with Py17XL parasites, and leukocytes removed by passage over microcrystalline cellulose columns. Total RNA was isolated using the guanidium isothiocyanate method, and mRNA isolated using oligo(dT)-cellulose chromatography.

First strand cDNA synthesis was completed using a 50-base primer and reverse transcriptase in the presence of 5-methyl dCTP. After second strand synthesis, uneven termini were treated with Pfu DNA polymerase and EcoRI adaptors ligated to the blunt ends. The sample was cleaved with XhoI and separated on a Sephacryl S-500 column.

Size-fractionated cDNA was precipitated and ligated to HybriZAP arms directionally using EcoRI-XhoI cleaved arms. After packaging, the phagemid vector (PAD-GAL4) was excised from the HybriZAP vector and plasmid DNA isolated."

BASE COUNT 315 a 81 c 121 g 229 t

ORIGIN

Alignment Scores:

Pred. No.: 4.32e-37 Length: 746
Score: 389.50 Matches: 76
Percent Similarity: 73.97% Conservative: 32
Best Local Similarity: 52.05% Mismatches: 35
Query Match: 53.43% Indels: 3
Gaps: 2

US-10-031-403-1 (1-146) x BM160783 (1-746)

QY 1 MetlaaglyleuthrProglugluAlaInTyrlsYlsAlaPheSerAlaVal 20

Db 125 ATGCAGACAGAGTTAAAGCAAGCAATTTCTGAATTCAGAAAGACGTTTCAGTTT 184

QY 21 AsphraspglyasnnglyThrIleasnlaaglInuaglyAlaIleuLysAlaThr 40

Db 185 GATTAAGATGAGATGAGACCATTAACAACAAGAAAGAGTACTGTCATCGATCGTTG 244

QY 41 GlyLysasnLeuSerGluAlaGlnLeuArgLysLeuSerGluValAspSerAspGly 60

Db 245 GGACAAACCAACGAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 304

XX WPI; 2002-241625/29.
DR Predicting toxic effects of compounds or the progression of these toxic
XX effects by determining the changes in gene expression in tissues or
PT cells exposed to the toxin and comparing these to gene expression in
PT unexposed tissues or cells.
PS Claim 1; Seq ID No 1352; 239pp; English.
XX
XX The invention relates to methods for predicting toxic effects of
CC compounds or the progression of these toxic effects by determining the
CC global changes in gene expression in tissues or cells exposed to the
CC toxin and comparing these to gene expression in unexposed tissues or
CC cells. Also included are methods of predicting at least one toxic
CC effect of a compound or progression of a toxic effect, preferably the
CC hepatotoxicity of a compound, comprising detecting the level of
CC expression in a tissue or cell sample exposed to the compound of two or
CC more genes listed in the specification, where differential expression of
CC the genes is indicative of at least one toxic effect or progression.
CC The method can also be used to identify an agent which modulates the
CC toxic response and predict cellular pathways that a compound modulates
CC in a cell. The methods utilise a set of at least two probes (on a solid
CC support in kit form), where each of the probes comprises a sequence that
CC specifically hybridises to a gene listed in the specification, a computer
CC system comprising a database containing information identifying the
CC expression level in a tissue or cell sample exposed to a hepatotoxin of a
CC set of genes comprising at least two genes listed in the specification,
CC and a user interface to view the information used to present information
CC identifying the expression level in a tissue or cell of at least one gene
CC listed in the specification. The method is useful for elucidating global
CC changes in gene expression and for identifying toxicity markers in
CC tissues or cell exposed to a known toxin. The genes may be used as
CC toxicity markers in drug screening and toxicity assays. The genes and
CC gene expression information may be used as diagnostic markers for the
CC prediction or identification of the physiological state of tissue or cell
CC sample that has been exposed to a compound or agent. Hepatotoxicity
CC is characterised by centrilobular necrosis and steatosis. The present
CC sequence is an expressed sequence tag (EST) or cDNA derived from a gene
CC which is differentially expressed in response to a hepatotoxic agent.
XX
SQ Sequence 654 BP; 214 A; 153 C; 159 G; 128 T; 0 other;
Alignment Scores:
Pred. No.: 1.89e-33 Length: 654
Score: 384.50 Matches: 76
Percent Similarity: 73.97% Conservative: 32
Best Local Similarity: 52.05% Mismatches: 35
Query Match: 52.74% Indels: 3
DB: 24 Gaps: 2
US-10-031-403-1 (1-146) x ABR63445 (1-654)
OY 1 MetAlaGlyLeuThrProGluAlaGlnIleAspGlyLeuGlnProLeuProGlnGlu 20
DB 112 ATGCGCTGATGACTGACTGAGAACAGATGCTGATTCAGAGAGCTTCTCCCTATT 171
OY 21 AspThrAspGlyAsnGlyThrIleAsnAlaGlnIleuGlyAlaAlaLeuAlaThr 40
DB 172 GATAAAGATGGCGGCGACCATCAACAAGAGAGCTGGGACTGTCATCGGCTCACTG 231
OY 41 GlyAsnLeuSerGluAlaGlnLeuArgLysLeuIleSerGluValAspSerAspGly 60
DB 232 GGTCAAGAACCAACAGACGCTGAACTGCAAGATGATCAACGAGTGATGCCGACGG 291
OY 61 AspGlyLeuIleSerPheGlnGluPheLeuThr---AlaAlaArgLysAlaArg----- 77
DB 292 AATGGCCACCTTGAATCTCCAGAGCTTGTGATGTGATGAGAAAATGAAGACACA 351
OY 78 AlaGlyLeuGluAspLeuGlnValAlaPheArgAlaPheAspGlnAspGlyAspGlyHis 97
DB 352 GATAGCGAAGAAATCCGTGAGGCGATTCGAGCTTTGACAAGAGATGCCAATGCCCTAC 411

OY 98 IleThrValAspGluLeuArgArgAlaMetAlaGlyLeuGlnProLeuProGlnGlu 117
DB 412 ATCAGTCGGCGAGAACTGCGGCGCATGACAAACCTCGGGGAAAGCTAAGCATGAA 471
OY 118 GluLeuAspAlaMetIleArgGluAlaAspValAspGlnAspGlyValAspGlyGlu 137
DB 472 GAAGTAGACGAAATGATCAACAGAAAGCAAGATATGATGAGACGAGCTCAACTAGAA 531
OY 138 GluPheAlaArgMetLeu 143
DB 532 GAATTCGTACAGATGATG 549

Search completed: May 16, 2003, 03:47:52
Job time : 254 secs

QY 1 MetAlaGlyLeuThrProGluGluAlaGlnTrpLysLysAlaPheSerAlaVal 20
 DB 58 ATGGCGTACAGCTGACTGACAGAGATGCGAGATTCAGAGAGCCCTTCCCTTT 117
 QY 21 AspThrAspGlyAsnGlyThrIleAsnAlaGlnGluLeuGlyAlaAlaLeuLysAlaThr 40
 DB 118 GCAAGGATGGAGATGGCTACTATCCACCACCAAGAGAGTGGGCACTGATGATGATCCCTG 177
 QY 41 GlyLysAsnLeuSerGluAlaGlnLeuArgLysLeuIleSerGlnValAlaPheSerAspGly 60
 DB 178 GCAAGAACCCCACTGAAACAGAGCTGCGAGATATGATCAATGAGTGGATGCGATGGG 237
 QY 61 AspGlyGluIleSerPheGlnGluPheLeuThr---AlaAlaArgLysAlaArg----- 77
 DB 238 AACGGACCATTCGATCCCGGAGTCCGACCATGATGGCCGAAGAATGAAGACACA 297
 QY 78 AlaGlyLeuGluAspLeuGlnValAlaPheArgAlaPheAspGlnAspGlyAspGlyHis 97
 DB 298 GACAGTGAAGAGAGATCCGAGAGGCGCTTCCTGCTTGCACAAAGATGGAGATGGCTAC 357
 QY 98 IleThrValAspGluLeuArgArgAlaMetAlaGlyLeuGlnProLeuProGlnGlu 117
 DB 358 ATCAGCGCCGCAAGCTGCTGCTACCTAATGACGAACCTGGGGAGAGCTGACCGATGAG 417
 QY 118 GluLeuAspAlaMetIleArgGluAlaAspValAspGlnAspGlyArgValAsnTrpGlu 137
 DB 418 GAGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAA 477
 QY 138 GluPheAlaArgMetLeu 143
 DB 478 GAGTTGTACAGATGATG 495
 RESULT 14
 AA004332
 ID AA004332 standard; DNA; 654 BP.
 AC AA004332;
 XX
 DT 27-SEP-1990 (first entry)
 XX
 DE Plasmid pRCM1 and gene for construction of calmodulin expression vector.
 XX
 KW Calmodulin; ds.
 XX
 OS Rattus rattus.
 XX
 PN -JPO2092286-A.
 XX
 PD 03-APR-1990.
 XX
 PF 30-SEP-1988; 88JP-0246239.
 XX
 PR 30-SEP-1988; 88JP-0246239;
 XX
 PA (KIRI) KIRIN BREWERY KK.
 XX
 DR WPI; 1990-144900/19.
 XX
 PT Calmodulin prepn. - by culturing transformed E. coli.
 XX
 PS Disclosure; ; P; Japanese.
 XX
 CC The plasmid is cut with HindIII and XbaI and inserted into a cloning
 CC site in pCALM1. The resulting plasmid, pCALM7 can be cut and ligated
 CC to AflIII/BamHI cut pS16311 to produce the expression plasmid pTCAL7.
 CC See also AA004331-4.
 XX
 SQ Sequence 654 BP; 214 A; 153 C; 159 G; 128 T; 0 other;

Alignment Scores: 1.89e-33 Length: 654
 Score: 384.50 Matches: 76

Percent Similarity: 73.97% Conservative: 32
 Best Local Similarity: 52.05% Mismatches: 35
 Query Match: 52.74% Indels: 3
 DB: 11 Gaps: 2
 US-10-031-403-1 (1-146) x AA004332 (1-654)
 QY 1 MetAlaGlyLeuThrProGluGluAlaGlnTrpLysLysAlaPheSerAlaVal 20
 DB 112 ATGGCGTACAGCTGACTGACAGAGATGCGAGATTCAGAGAGCCCTTCCCTATT 171
 QY 21 AspThrAspGlyAsnGlyThrIleAsnAlaGlnGluLeuGlyAlaAlaLeuLysAlaThr 40
 DB 172 GATAAAGATGGGAGACGCGACATCAACAAGAGAGCTGGGCACTGATGCGCTACCTG 231
 QY 41 GlyLysAsnLeuSerGluAlaGlnLeuArgLysLeuIleSerGlnValAlaPheSerAspGly 60
 DB 232 GGTCAAGAACCCCAAGAGCTGAACTGACAGATATGATCAACGAGTGGATGCGAGGG 291
 QY 61 AspGlyGluIleSerPheGlnGluPheLeuThr---AlaAlaArgLysAlaArg----- 77
 DB 292 AATGGACCATTCGATCCCGGAGTCCGACCATGATGCTGAAATAATGAAGACACA 351
 QY 78 AlaGlyLeuGluAspLeuGlnValAlaPheArgAlaPheAspGlnAspGlyAspGlyHis 97
 DB 352 GATAGCGAAGAAGAAATCCGTGAGCGATTCGAGTCTTGACAAAGATGGCAATGGCTAC 411
 QY 98 IleThrValAspGluLeuArgArgAlaMetAlaGlyLeuGlnProLeuProGlnGlu 117
 DB 412 ATCAGTGGCGCAAGCTGCGCCACGTCATGACAAACCTGGGGAGAGCTGACAGATGAA 471
 QY 118 GluLeuAspAlaMetIleArgGluAlaAspValAspGlnAspGlyArgValAsnTrpGlu 137
 DB 472 GAGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAA 531
 QY 138 GluPheAlaArgMetLeu 143
 DB 532 GATTCGTACAGATGATG 549
 RESULT 15
 ABR63445
 ID ABR63445 standard; cDNA; 654 BP.
 AC ABR63445;
 XX
 DT 18-JUN-2002 (first entry)
 XX
 DE Rat sequence differentially expressed in response to a hepatotoxin #1352.
 XX
 KW Rat; ss; hepatotoxin; expressed sequence tag; EST; drug screening;
 KW differential expression; centrilobular necrosis; steatosis.
 XX
 OS Rattus norvegicus.
 XX
 PN W0200210453-A2.
 XX
 PD 07-FEB-2002.
 XX
 PF 30-JUL-2001; 2001WO-US23872.
 XX
 PR 31-JUL-2000; 2000US-222040P.
 XX
 PR 02-NOV-2000; 2000US-244880P.
 XX
 PR 11-MAY-2001; 2001US-290029P.
 XX
 PR 15-MAY-2001; 2001US-290645P.
 XX
 PR 22-MAY-2001; 2001US-292336P.
 XX
 PR 06-JUN-2001; 2001US-295798P.
 XX
 PR 13-JUN-2001; 2001US-297457P.
 XX
 PR 19-JUN-2001; 2001US-298884P.
 XX
 PR 09-JUL-2001; 2001US-303459P.
 XX
 PA (GENE-) GENE LOGIC INC.
 XX
 PI Mendrick D, Porter MW, Johnson KR, Castle AL, Elashoff MR;

Db 404 GAAGTTGATGAATGATCAGGAGACAGATATTGATGTGATGTCATGAATAATATGAA 463
 QY 138 Gluphealarqmetleu 143
 ||||| :|||:
 Db 464 GAGTTTGTACAAATGATG 481

RESULT 12
 AAQ04334
 ID AAQ04334 standard; DNA; 504 BP.
 XX
 AC AAQ04334;
 XX
 DT 27-SEP-1990 (first entry)
 XX
 DE Plasmid pOCAL7 contg. gene for calmodulin.
 XX
 KM Calmodulin; ds.
 XX
 OS Rattus rattus.
 XX
 PN JP02092286-A.
 XX
 PD 03-APR-1990.
 XX
 PF 30-SEP-1988; 88JP-0246239.
 XX
 PR 30-SEP-1988; 88JP-0246239.
 XX
 PA (KIRI) KIRIN BREWERY KK.
 XX
 DR WPI; 1990-144900/19.
 XX
 PT Calmodulin prepn. - by culturing transformed E. coli.
 XX
 PS Disclosure; P; Japanese.
 XX
 CC The plasmid, pOCAL7, can be cut and ligated to AflII/BamHI cut
 CC pST6311 to produce the expression plasmid pTCAI7.
 CC See also AAQ04331-3.
 CC
 XX SQ Sequence 504 BP; 170 A; 102 C; 131 G; 101 T; 0 other;

Alignment Scores:
 Pred. No.: 1,38e-33 Length: 504
 Score: 384.50 Matches: 76
 Percent Similarity: 73.97% Conservative: 32
 Best Local Similarity: 52.05% Mismatches: 35
 Query Match: 52.74% Indels: 3
 DB: 11 Gaps: 2

US-10-031-403-1 (1-146) x AAQ04334 (1-504)

QY 1 MetalaglyleuethrproglugluaglntrlysalaapheserAlaVal 20
 ||||| :|||:
 Db 17 ATGGCAGATCAATTACAGAGAGAACAGATCGCTGAATTCAGAGAGCTTTCTCCCTATT 76
 QY 21 AspThrAspGlyasnnglythrIleasnAlaglnleuGlyAlaalaLeuysAlaThr 40
 ||| :|||:
 Db 77 GATTAAGATGGGAGCGGACCATCACAAAGAGAGCTGGGACTGTCATGCGGTCAC 136
 QY 41 GlyAsnleuSerGluAlaglnleuArgLysleuIleSerGluValaIaSerAspGly 60
 ||||| :|||:
 Db 137 GGTACAGAACCCACAGACGAGCTGAGATGATGATCAACGAGGTGATGCCGAGCGG 196
 QY 61 AspGlyIleuIleSerPheGlnGluPheLeuThr---AlaAlaArgLysAlaArg----- 77
 :||| :|||:
 Db 197 AATGGCAGCATGTGACCTCCAGAGTTCTTACATGATGCTAGAAAAGAAAGACACA 256
 QY 78 AlaglyleuGlnAspLeuGlnValAlaIaPheArgAlaPheAspGlnAspGlyHis 97
 ||||| :|||:
 Db 257 GATAGCAGCAAGAGAAATCCGTGAGGCAATCCGAGTCTTACACAAGATGCAATGCGCTAC 316
 QY 98 IleThrValaspGluLeuArgArgAlaMetAlaglyleuGlnProLeuProGlnGln 117

Db 317 ATCAGTCGGCAGAACTGCGCCAGCTCATGACAAACCTCGGGGAAAGCTAACAGATGAA 376
 ||||| :|||:
 QY 118 GluleuAspAlaMetIleArgGluAlaAspValaIaAspGlnAspGlyValaIaArgTyrGlu 137
 ||||| :|||:
 Db 377 GAAGTAGCAGCAAAATGATCAGAGAGAGATATTGATGAGAGCGAGGTCACACTATGAA 436

QY 138 Gluphealarqmetleu 143
 ||||| :|||:
 Db 437 GAATTCCTACAGATGATG 454

RESULT 13
 AAC03838
 ID AAC03838 standard; cDNA; 564 BP.
 XX
 AC AAC03838;
 XX
 DT 06-OCT-2000 (first entry)
 XX
 DE Human secreted protein 5' EST, SEQ ID NO: 3836.
 XX
 KM Human: 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
 KM gene therapy; chromosome mapping; ss.
 XX
 OS Homo sapiens.
 XX
 PN EP1033401-A2.
 XX
 PD 06-SEP-2000.
 XX
 PF 21-FEB-2000; 2000EP-0200610.
 XX
 PR 26-FEB-1999; 99US-0122487.
 XX
 PA (GEST) GENSET.
 XX
 DR Dumas Milne Edwards J, Duclert A, Giordano J;
 DR WPI; 2000-500381/45.
 DR P-PADB; AAC03832.
 XX

New nucleic acid that is a 5' expressed sequence tag (5' EST) for
 obtaining cDNAs and genomic DNAs that correspond to 5' ESTs and for
 diagnostic, forensic, gene therapy and chromosome mapping procedures -
 Claim 1; SEQ ID 3836; 71pp + CD-ROM; English.

The present sequence is one of a large number of 5' ESTs derived from
 cDNAs encoding secreted proteins. An ORF has been identified within the
 sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs
 derived from 30 different tissues. EST sequences usually correspond
 mainly to the 3' untranslated region (UTR) of the mRNA because they are
 often obtained from oligo-dT primed cDNA libraries. Such ESTs are not
 well suited for isolating cDNA sequences derived from the 5' ends of
 cDNAs and even in those cases where longer cDNA sequences have been
 obtained, the full 5' UTR is rarely included. 5' ESTs are derived from
 cDNAs with intact 5' ends and can therefore be used to obtain full length
 cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic,
 gene therapy and chromosome mapping procedures. They are used to obtain
 upstream regulatory sequences and to design expression and secretion
 vectors.

Sequence 564 BP; 146 A; 119 C; 191 G; 108 T; 0 other;

Alignment Scores:
 Pred. No.: 1,58e-33 Length: 564
 Score: 384.50 Matches: 76
 Percent Similarity: 73.97% Conservative: 32
 Best Local Similarity: 52.05% Mismatches: 35
 Query Match: 52.74% Indels: 3
 DB: 21 Gaps: 2

US-10-031-403-1 (1-146) x AAC03838 (1-564)

CC using primers AA095553-4 to PCR amplify the coding region. The coding
 CC region of the gene was inserted into the plasmids pMAL(RT)-2, pRIZT
 CC and pGEX-5X-1 to generate plasmids pMALCAM (AA095550), pPRACAM (AA095551)
 CC and pGSMCAM (AA095552) respectively. These plasmids express maltose-
 CC (AA078524), protein A- (AA078525) and
 CC glutathione-S-transferase-calmodulin (AA078526) fusion proteins,
 CC respectively. The fusion proteins produced retain the same activity as
 CC calmodulin as measured by the phosphodiesterase activating method. The
 CC fusion protein, which can be obtained at high purity, can be used to
 CC isolate calmodulin binding proteins, measure their activity and screen
 CC for calmodulin inhibitors.

XX SQ Sequence 450 BP; 167 A; 61 C; 115 G; 107 T; 0 other:

Alignment Scores:
 Pred. No.: 1,21e-33 Length: 450
 Score: 384.50 Matches: 76
 Percent Similarity: 73.97% Conservative: 32
 Best Local Similarity: 52.05% Mismatches: 35
 Query Match: 52.74% Indels: 3
 DB: 16 Gaps: 2

US-10-031-403-1 (1-146) x AA095549 (1-450)

OY 1 MetAlaGlyGluLeuThrProGluGluAlaGlnTyrLysLysAlaPheSerAlaVal 20
 DB 1 ATGGCTGACCACTGCTGCAAGAGCGAGATTGCAAGATTCAAGAACCTTTTCACATATT 60
 OY 21 AspThrAspGlyAsnGlyThrIleAsnAlaGlnGluLeuGlyAlaIleLeuLysAlaThr 40
 DB 61 GACAAAGATGGTGGATGGAATTAACACAAAGAAATTTGGAACTGTAATGACATCTCTT 120
 OY 41 GlyLysAsnLeuSerGluAlaGlnLeuArgLysLeuIleSerGluValAspSerAspGly 60
 DB 121 GGGCAGAAATCCCAAGAACAGACAGATTACAGACATGATTAAGAACTAGATGCTATG 180
 OY 61 AspGlyGluIleSerPheGlnGluPheLeuThr---AlaAlaArgLysAlaArg----- 77
 DB 181 AATGGCAATGACTTCCTGCAATTTCTGACATGATGCAAGAAATTTGAAGACACACA 240
 OY 78 AlaGlyLeuGluAspLeuGlnValAlaPheArgAlaPheAspGlnAspGlyAspGlyHis 97
 DB 241 GACAGTGAAGAAATTTAGACAGCATTCCTGCTGTGATTAAGATGCGATGCTAT 300
 OY 98 IleThrValAspGluLeuArgAlaMetAlaGlyLeuGlyGlnProLeuProGlnGlu 117
 DB 301 ATTAGTGTGACAGAACTGCGCATGTGATGACAAACCTTGGAGAGAAATTAAACAGATGA 360
 OY 118 GluLeuAspAlaMetIleArgGluAlaAspValAspGlnAspGlyArgValAsnTyrGlu 137
 DB 361 GAAGTGTGAATGATGTCAGGAGACAGATATTGATGTGATGATGCTCAACTAACTATGAA 420
 OY 138 GluPheAlaArgMetLeu 143
 DB 421 GAGTTTGTACAAATGATG 438

XX RESULT 11

XX ABK44905 standard; cDNA; 485 BP.

XX AC ABK44905;

XX 05-JUN-2002 (first entry)

XX DE cDNA encoding colon tumour protein, SEQ ID NO 456.

XX Human; colon tumour; vaccine; colon cancer; immunogenic;

XX Immunotherapy; gene; ss.

XX Homo sapiens.

XX WO200212328-A2.

PD 14-FEB-2002.

XX 31-JUL-2001; 2001WO-US24218.

XX 03-AUG-2000; 2000US-223283P.

XX 28-MAR-2001; 2001US-279763P.

XX 29-JUN-2001; 2001US-302051P.

XX (CORI-) CORIXA CORP.

XX King GE, Meagher MJ, Xu J, Secretist H;

XX WPI: 2002-241739/29.

XX New colon cancer polypeptides and polynucleotides, useful as vaccines,
 PT for diagnosing, preventing, and treating colon cancer, and as markers
 PT for the progression of cancer -

PS Claim 1; SEQ ID NO 456; 147bp; English.

CC The invention relates to polynucleotides encoding colon tumour proteins.
 CC The polynucleotides and encoded polypeptides are useful in pharmaceutical
 CC compositions, such as vaccines, for the diagnosis, prevention, and
 CC treatment of colon cancer. Polynucleotide sequences may be used as
 CC hybridisation probes or primers, and in the design and preparation of
 CC ribozyme molecules for inhibiting expression of tumour polypeptides and
 CC proteins in tumour cells. The compositions are useful for stimulating an
 CC immune response against cancer, particularly for the immunotherapy of
 CC colon cancer, and as markers for the progression of cancer.
 CC ABK4450-ABK46237 represent coding sequences of human colon tumour
 CC proteins of the invention.
 CC Note: With the exception of SEQ ID No 1 and 2, the sequence data
 CC for this patent did not form part of the printed specification but was
 XX supplied by the European Patent Office.

XX SQ Sequence 485 BP; 168 A; 69 C; 130 G; 118 T; 0 other:

Alignment Scores:
 Pred. No.: 1,32e-33 Length: 485
 Score: 384.50 Matches: 76
 Percent Similarity: 73.97% Conservative: 32
 Best Local Similarity: 52.05% Mismatches: 35
 Query Match: 52.74% Indels: 3
 DB: 24 Gaps: 2

US-10-031-403-1 (1-146) x ABK44905 (1-485)

OY 1 MetAlaGlyGluLeuThrProGluGluAlaGlnTyrLysLysAlaPheSerAlaVal 20
 DB 44 ATGGCTGACCACTGCTGCAAGAGCGAGATTGCAAGATTCAAGAACCTTTTCACATATT 103
 OY 21 AspThrAspGlyAsnGlyThrIleAsnAlaGlnGluLeuGlyAlaIleLeuLysAlaThr 40
 DB 104 GACAAAGATGGTGGATGGAATTAACACAAAGAAATTTGGAACTGTAATGACATCTCTT 163
 OY 41 GlyLysAsnLeuSerGluAlaGlnLeuArgLysLeuIleSerGluValAspSerAspGly 60
 DB 164 GGGCAGAAATCCCAAGAACAGACAGATTACAGACATGATTAAGAACTAGATGCTATG 223
 OY 61 AspGlyGluIleSerPheGlnGluPheLeuThr---AlaAlaArgLysAlaArg----- 77
 DB 224 AATGGCAATGACTTCCTGCAATTTCTGACATGATGCAAGAAATTTGAAGACACACA 283
 OY 78 AlaGlyLeuGluAspLeuGlnValAlaPheArgAlaPheAspGlnAspGlyAspGlyHis 97
 DB 284 GACAGTGAAGAAATTTAGACAGCATTCCTGCTGTGATTAAGATGCGATGCTAT 343
 OY 98 IleThrValAspGluLeuArgAlaMetAlaGlyLeuGlyGlnProLeuProGlnGlu 117
 DB 344 ATTAGTGTGACAGAACTGCGCATGTGATGACAAACCTTGGAGAGAAATTAAACAGATGA 403
 OY 118 GluLeuAspAlaMetIleArgGluAlaAspValAspGlnAspGlyArgValAsnTyrGlu 137

Best Local Similarity: 96.408
Query Match: 72.578
DB: 21

Mismatches: 4
Indels: 0
Gaps: 0

US-10-031-403-1 (1-146) x AAF21853 (1-497)

QY 1 MetAlaGlyLeuThrProGluGluAlaGlnTyrLysLysAlaPheSerAlaVal 20
DB 136 ATGGCCGCTAGCTGACCTCTGAGAGAGAGCCAGTACAAAAGGCTTCTCCGCGGT 195
QY 21 AspThrAspGlyAsnGlyThrIleAsnAlaGlnGluLeuGlyAlaAlaLeuLysAlaThr 40
DB 196 GACACGATGAAAGCGCACATCAATGCGCAGAGCTGGCGGCGCTGAAAGCCAGC 255
QY 41 GLYAsnLeuSerGlnAlaGlnLeuArgLysLeuIleSerGluValAspSerAspGly 60
DB 256 GGCAGAACTCTCGAGGCGCCAGCTAAGAACTCTCCGAGTTGACRGCAGCGC 315
QY 61 AspGlyLysLeuSerPheGlnGluPheLeuThrAlaAlaArgLysAlaArgAlaGlyLeu 80
DB 316 GACGCGCAATCAAGCTTCCAGAGATTCTGACGCGCGRAGAAAGCCAGCGCGCTG 375
QY 81 GluAspLeuValAlaAlaPheArgAlaPheAspGlnAspGlyHisIleThrVal 100
DB 376 GAGGACCTGCAAGTCCGCTTCCGCGCTTCCGACAGAGTGGCAGCGCACATCACCGTG 435
QY 101 AspGluLeuArgArgAlaMetAlaGlyLeuGly 111
DB 436 GACGAGCTCAGCGCGGCATCGCGGGGTGGG 468

RESULT 9

AA04331
ID AA04331 standard; cDNA; 447 BP.

AC AA04331;

DT 27-SEP-1990 (first entry)

DE Recombinant calmodulin gene.

XX Calmodulin; ss.

OS Rattus rattus.

XX JP02092286-A.

XX 03-APR-1990.

XX PF 30-SEP-1988; 88JP-0246239.

XX PR 30-SEP-1988; 88JP-0246239.

XX (KIRI) KIRIN BREWERY KK.

DR WPI: 1990-144900/19.

DR P-PSDB; AAR04583.

PT Calmodulin prepn. - by culturing transformed E. coli.

PS Claim 1; Fig 1; 10pp; Japanese.

XX The sequence can be subcloned and used to construct a vector for the

CC expression of calmodulin.

CC See also AA04332-4.

XX SQ Sequence 447 BP; 155 A; 87 C; 122 G; 83 T; 0 other;

Alignment Scores:

Pred. No.: 1.2e-33
Score: 384.50
Percent Similarity: 73.97%
Best Local Similarity: 52.05%
Query Match: 52.74%

Length: 447
Matches: 76
Conservative: 32
Mismatches: 35
Indels: 3

DB: 11 Gaps: 2
US-10-031-403-1 (1-146) x AA04331 (1-447)

QY 1 MetAlaGlyLeuThrProGluGluAlaGlnTyrLysLysAlaPheSerAlaVal 20
DB 1 ATGGCAGATCAATTAACAGAGACAGATGCTGAATTCAAAAGAGCTTCTCCCTATT 60
QY 21 AspThrAspGlyAsnGlyThrIleAsnAlaGlnGluLeuGlyAlaAlaLeuLysAlaThr 40
DB 61 GATTAAGATGGGACCGCACCATCAACAAGAGCTGGGAGCTGCATGCGTCACTG 120
QY 41 GLYAsnLeuSerGlnAlaGlnLeuArgLysLeuIleSerGluValAspSerAspGly 60
DB 121 GGTCAAGAACCAACAGAGGCTGAAGCTCAGAGATATGATCAACGAGGTGATGCCAGCGG 180
QY 61 AspGlyLysLeuSerPheGlnGluPheLeuThr--AlaAlaArgLysAlaArg----- 77
DB 181 AATGGCACATTTGACTTCCAGAGTCTTGACTATGATGGCTAGCAAAAATGAAAGACACA 240
QY 78 AlaGlyLeuGluAspLeuGlnValAlaPheArgAlaPheAspGlnAspGlyAspGlyHis 97
DB 241 GATAGCCAGAGAAATCCGTCGAGGCAATTCGAGCTTTGACAAAGATGGCAATGCTTAC 300
QY 98 IleThrValAspGluLeuArgArgAlaMetAlaGlyLeuGlnGluProLeuProGlnGlu 117
DB 301 ATCAGTCCGCGCAAGTCCGCGCACGTCATGACAAACCTCGGGGAAAGCTTAACAGATGAA 360
QY 118 GluLeuAspAlaMetIleArgGluAlaAspValAspGlnAspGlyArgValAsnTyrGlu 137
DB 361 GAAGTAGACGAATGATCAGAGAGAGACAGATATGATGAGACGAGCGATCAACTATGAA 420
QY 138 GluPheAlaArgMetLeu 143
DB 421 GAATTGCTACAGATGATG 438

RESULT 10

AA095549
ID AA095549 standard; cDNA to mRNA; 450 BP.

AC AA095549;

DT 31-JAN-1996 (first entry)

XX Human calmodulin cDNA sequence.

XX Human: calmodulin; fibrosarcoma cell; primer: PCR: amplification;

XX maltose; protein A; glutathione-S-transferase; fusion protein; activity;

XX phosphodiesterase activating method; binding protein; inhibitor; ds.

XX Homo sapiens.

XX JP07126297-A.

XX 16-MAY-1995.

XX 05-NOV-1993; 93JP-0299041.

XX 05-NOV-1993; 93JP-0299041.

PA (SAGA) SAGAMI CHEM RES CENTRE.

DR WPI: 1995-212960/28.

DR P-PSDB; AAR78523.

PT Fusion of calmodulin (CAM) with specific binding peptide - has same

PT activity as CAM, useful for screening for CAM inhibitors, measuring

PT CAM binding protein activity, etc.

XX Examples; Page 5-6; 12pp; Japanese.

XX The nucleotide sequence of the human calmodulin cDNA clone pKAL-CAM.

XX The clone was isolated from the human fibrosarcoma cell line HT-1080

PR 05-JAN-2001: 2001US-0259678.
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX
 PA Rosen CA, Barash SC, Ruben SM;
 XX WPI: 2001-488781/53.
 DR P-PSDB: AAM43549.
 XX
 XX New isolated nucleic acids and polypeptides, useful for diagnosing,
 PT treating and/or preventing human diseases and disorders -
 XX
 PS Claim 1: SEQ ID NO 63: 664pp + Sequence Listing; English.
 XX

CC The invention relates to human polynucleotides (AA163803-AA164012) and
 CC the encoded proteins (AAM434497-AAM43660) useful for preventing, treating
 CC or ameliorating medical conditions e.g. by protein or gene therapy. The
 CC genes were isolated from a range of human tissues disclosed in the
 CC specification. The nucleic acids, proteins, antibodies and (ant)agonists
 CC are useful in the diagnosis, treatment and prevention of: (a) cancer,
 CC e.g. breast and ovarian cancer and other cancers of the adrenal gland,
 CC bone, bone marrow, breast, gastrointestinal tract, liver, lung, or
 CC urogenital; (b) immune disorders e.g. Addison's disease, allergies,
 CC autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus,
 CC Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative
 CC colitis; (c) cardiovascular disorders such as myocardial ischaemia;
 CC (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and
 CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
 CC and parasitic infections.
 CC Note: The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
 XX

XX Sequence 920 BP; 197 A; 274 C; 313 G; 135 T; 1 other;

Alignment Scores:

Pred. No.:	1,79e-70	Length:	920
Score:	722.00	Matches:	144
Percent Similarity:	99.32%	Conservative:	1
Best Local Similarity:	98.63%	Mismatches:	1
Query Match:	99.04%	Indels:	0
DB:	22	Gaps:	0

US-10-031-403-1 (1-146) x AAI63855 (1-920)

OY 1 MetAlaGluGluLeuThrProGluGluGluAlaGluTyrTylsYsAlaPheSerAlaVal 20
 DB 137 ATGGCCGGGAGCTGACTCTGAGGAGAGGCCCAATACAAAGGCTTTCTCCGGGTT 196
 OY 21 AspThrAspGlyAsnGlyThrIleAsnAlaGluGluGluGluGluGluGluGluGluGlu 40
 DB 197 GACACGAGTGAAGAACGCGACCATCATGCGGAGGAGGCGGCGCGCGCGGAGGCGACG 256
 OY 41 GlyValAspLeuSerGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 60
 DB 257 GGCACAAACCTCTCGAGGAGCCAGTAAAGGAACTATCTCGAGGTTGACRCGCGCGG 316
 OY 61 AspGlyGluIleSerPheGluGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 80
 DB 317 GACGGGGAATCAGCTTCAGAGGTTCTGACGCGGCGGCGGAGAGGCGGCGGCGGCTG 376
 OY 81 GluAspLeuGluValAlaPheArgAlaPheAspGluAspGlyAspGlyIleThrVal 100
 DB 377 GAGGACCTCAGAGTCCCTTCGCGGCTTCGACAGAGATGGCGACGCGCACATCACCGTG 436
 OY 101 AspGluLeuArgAlaMetAlaGlyLeuGlyGluProLeuProGluGluGluGluGluGlu 120
 DB 437 GACGACCTCAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 496
 OY 121 AlaMetIleArgGluAlaAspValAspGluAspGlyArgValAspThrGluGluPheAla 140
 DB 497 GCCATGATCCGGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 556

OY 141 ArgMetLeuAlaGluGlu 146
 DB 557 AGGATGCTCGCCCGAGAG 574

RESULT 8
 AAF21853

ID AAF21853 standard; DNA; 497 BP.

AC AAF21853;

DT 27-MAR-2001 (first entry)

XX Human breast and ovarian cancer associated antigen gene SEQ ID 240.

XX Human: breast cancer; cytostatic; immunosuppressive;
 KW neurotropic; neuroprotective; antiviral; antiallergic; hepatotropic;
 KW antidiabetic; antiinflammatory; anticancer; vulnary; anticonvulsant;
 KW antibacterial; antifungal; antiparasitic; cardiant; immune disorder;
 KW Addison's disease; allergy; autoimmune haemolytic anaemia;
 KW autoimmune thyroiditis; diabetes mellitus; Crohn's disease;
 KW multiple sclerosis; rheumatoid arthritis; ulcerative colitis;
 KW cardiovascular disorder; wound healing; neurological disease; ds.

XX Homo sapiens.

PN WO20005173-A1.

PD 21-SEP-2000.

PF 08-MAR-2000: 2000MO-US05881.

PR 12-MAR-1999: 99US-0124270.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Rosen CA, Ruben SM;

XX WPI: 2000-611515/58.

XX P-PSDB: AAB58950.

PT New human breast and ovarian cancer associated gene sequences and the
 PT polypeptides encoded by these genes, useful in the prevention,
 PT treatment and diagnosis of cancer, immune disorders, cardiovascular
 PT disorders and neurological diseases -
 XX

PS Claim 1: Page 665; 1299pp; English.

CC Sequences AAF21614 - AAF22031 represent DNA sequences encoding human
 CC proteins AAB58711 - AAB59128. The DNA and protein sequences are
 CC associated with breast and ovarian cancer. Included in the invention are
 CC sequences AAF22032 - AAF22040 and AAB59129 which are used in the
 CC isolation and characterisation of the DNA and protein sequences of the
 CC invention. The breast and ovarian cancer associated DNA, protein, agonist
 CC or antagonist sequences exhibit cytostatic; immunosuppressive;
 CC neurotropic; neuroprotective; antiviral; antiallergic; hepatotropic;
 CC antidiabetic; antiinflammatory; anticancer; vulnary; anticonvulsant;
 CC antibacterial; antifungal; antiparasitic and cardiant activity. The
 CC polynucleotide and protein sequences are used in the diagnosis of cancer,
 CC particularly breast and ovarian cancer. The nucleic acid sequences,
 CC proteins, agonists and agonists may also be used in the diagnosis of
 CC prevention and treatment of immune disorders e.g. Addison's disease,
 CC allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis,
 CC diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid
 CC arthritis and ulcerative colitis; cardiovascular disorders such as
 CC myocardial ischaemia; wound healing; neurological diseases such as
 CC cerebral anoxia and epilepsy; and infectious diseases.

XX Sequence 497 BP; 100 A; 143 C; 176 G; 70 T; 8 other;

Alignment Scores:

Pred. No.:	1,61e-49	Length:	497
Score:	529.00 <td>Matches:</td> <td>107 </td>	Matches:	107
Percent Similarity:	96.40%	Conservative:	0

KW	antiparasitic; cardiant; gene therapy; cancer; immune disorder;	PR	25-SEP-2000;	2000US-0234997.
KW	cardiovascular disorder; neurological disease; infection; human; ss.	PR	25-SEP-2000;	2000US-0234998.
XX		PR	26-SEP-2000;	2000US-0235484.
OS	Homo sapiens.	PR	27-SEP-2000;	2000US-0235834.
XX		PR	27-SEP-2000;	2000US-0235836.
PN	MO200155308-A2.	PR	29-SEP-2000;	2000US-0236327.
XX		PR	29-SEP-2000;	2000US-0236367.
PD	02-AUG-2001.	PR	29-SEP-2000;	2000US-0236368.
XX		PR	29-SEP-2000;	2000US-0236369.
XX		PR	29-SEP-2000;	2000US-0236370.
XX		PR	02-OCT-2000;	2000US-0236802.
XX		PR	02-OCT-2000;	2000US-0237037.
XX		PR	02-OCT-2000;	2000US-0237038.
XX		PR	02-OCT-2000;	2000US-0237040.
XX		PR	13-OCT-2000;	2000US-0239935.
XX		PR	20-OCT-2000;	2000US-0240960.
XX		PR	20-OCT-2000;	2000US-0241221.
XX		PR	20-OCT-2000;	2000US-0241785.
XX		PR	20-OCT-2000;	2000US-0241787.
XX		PR	20-OCT-2000;	2000US-0241808.
XX		PR	20-OCT-2000;	2000US-0241809.
XX		PR	20-OCT-2000;	2000US-0241826.
XX		PR	01-NOV-2000;	2000US-0244617.
XX		PR	08-NOV-2000;	2000US-0246474.
XX		PR	08-NOV-2000;	2000US-0246475.
XX		PR	08-NOV-2000;	2000US-0246476.
XX		PR	08-NOV-2000;	2000US-0246477.
XX		PR	08-NOV-2000;	2000US-0246478.
XX		PR	08-NOV-2000;	2000US-0246523.
XX		PR	08-NOV-2000;	2000US-0246524.
XX		PR	08-NOV-2000;	2000US-0246525.
XX		PR	08-NOV-2000;	2000US-0246526.
XX		PR	08-NOV-2000;	2000US-0246527.
XX		PR	08-NOV-2000;	2000US-0246528.
XX		PR	08-NOV-2000;	2000US-0246532.
XX		PR	08-NOV-2000;	2000US-0246609.
XX		PR	08-NOV-2000;	2000US-0246610.
XX		PR	08-NOV-2000;	2000US-0246611.
XX		PR	17-NOV-2000;	2000US-0246613.
XX		PR	17-NOV-2000;	2000US-0249207.
XX		PR	17-NOV-2000;	2000US-0249208.
XX		PR	17-NOV-2000;	2000US-0249209.
XX		PR	17-NOV-2000;	2000US-0249210.
XX		PR	17-NOV-2000;	2000US-0249211.
XX		PR	17-NOV-2000;	2000US-0249212.
XX		PR	17-NOV-2000;	2000US-0249213.
XX		PR	17-NOV-2000;	2000US-0249214.
XX		PR	17-NOV-2000;	2000US-0249215.
XX		PR	17-NOV-2000;	2000US-0249216.
XX		PR	17-NOV-2000;	2000US-0249217.
XX		PR	17-NOV-2000;	2000US-0249218.
XX		PR	17-NOV-2000;	2000US-0249244.
XX		PR	17-NOV-2000;	2000US-0249245.
XX		PR	17-NOV-2000;	2000US-0249264.
XX		PR	17-NOV-2000;	2000US-0249265.
XX		PR	17-NOV-2000;	2000US-0249297.
XX		PR	17-NOV-2000;	2000US-0249299.
XX		PR	17-NOV-2000;	2000US-0249300.
XX		PR	01-DEC-2000;	2000US-0250160.
XX		PR	01-DEC-2000;	2000US-0250391.
XX		PR	05-DEC-2000;	2000US-0251030.
XX		PR	05-DEC-2000;	2000US-0251988.
XX		PR	05-DEC-2000;	2000US-0256719.
XX		PR	06-DEC-2000;	2000US-0251679.
XX		PR	08-DEC-2000;	2000US-0251856.
XX		PR	08-DEC-2000;	2000US-0251868.
XX		PR	08-DEC-2000;	2000US-0251869.
XX		PR	08-DEC-2000;	2000US-0251989.
XX		PR	08-DEC-2000;	2000US-0251990.
XX		PR	11-DEC-2000;	2000US-0254097.
XX		PR	25-SEP-2000;	2000US-0234997.
XX		PR	25-SEP-2000;	2000US-0234998.
XX		PR	26-SEP-2000;	2000US-0235484.
XX		PR	27-SEP-2000;	2000US-0235834.
XX		PR	27-SEP-2000;	2000US-0235836.
XX		PR	29-SEP-2000;	2000US-0236327.
XX		PR	29-SEP-2000;	2000US-0236367.
XX		PR	29-SEP-2000;	2000US-0236368.
XX		PR	29-SEP-2000;	2000US-0236369.
XX		PR	29-SEP-2000;	2000US-0236370.
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Db	135	ATGGCCCGTACCTGACTCCTCGAGGAGGAGGCCCACTACAAAAAGGCTTTCGCGGTT	194
OY	21	Asp1h1r1a1s1p1g1y1a1n1g1t1h1r1l1e1a1n1a1g1n1g1u1e1g1y1a1a1a1e1u1y1s1a1a1t1h1r	40
Db	195	GACACGGATGGAAACGGCACCATCATTCGCCAGAGACTGGCGCGGCGCTGAAGCCACAC	254
OY	41	G1y1y1s1a1n1e1u1s1e1r1g1u1a1g1n1e1u1a1g1y1s1e1u1l1e1s1e1r1g1u1a1a1s1p1e1r1a1s1p1y	60
Db	255	GGCAAGAACCTCTCGGAGGCCAGCTAAGAAACTCATCTCCGAGGTTGCACGCGACGCG	314
OY	61	Asp1y1l1u1l1e1s1e1r1p1h1e1g1n1g1u1p1h1e1u1t1h1r1A1a1A1a1r1y1s1a1a1r1a1g1a1g1e1u	80
Db	315	GAGCGCAAAATACACTTCACAGACTTCCTACAGCGCGCCGACAGAGCCACAGGCCCGGCTG	374
OY	81	G1u1a1s1p1e1u1c1u1a1a1a1p1h1e1a1g1a1p1h1e1a1s1p1a1s1p1y1a1s1p1y1h1l1e1t1h1r1a1	100
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OY	121	Ala1n1e1l1e1a1r1g1u1a1a1a1s1p1a1a1s1p1a1s1p1y1a1r1y1a1s1a1n1t1y1g1u1a1p1h1e1a1	140
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DT	05-JUN-2002	(first entry)	
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DE		DNA encoding novel central nervous system protein #488.	
XX			
KM		Central nervous system; CNS; autoimmune disease; rheumatoid arthritis	
KM		hyperproliferative disorder; neoplasm; cardiovascular disorder	
KM		cardiac arrest; cerebrovascular disorder; ischemia; angiogenesis;	
KM		nervous system disorder; Alzheimer's disease; AIDS; ocular disorder;	
KM		acquired immunodeficiency virus; dysphagia; gastrointestinal disorder;	
KM		adenocarcinoma; reproductive system disorder; testicular feminisation;	
KM		endocrine disorder; diabetes; cancer; leukemia; neovascularisation;	
KM		respiratory disorder; renal disorder; kidney failure; blood disorder;	
KM		myocardial infarction; wound healing; cell proliferation; skin aging;	
KM		food additive; food preservative; gene therapy; gene; ss.	
XX			
OS	Homo sapiens.		
XX			
PN	WO200155318-A2.		
XX			
PD	02-AUG-2001.		
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PE	17-JAN-2001;	2001WO-US01332.	
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PR 17-NOV-2000; 2000US-0249211.
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 PR 05-DEC-2000; 2000US-0251030.
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 PR 08-DEC-2000; 2000US-0251989.
 PR 11-DEC-2000; 2000US-0251990.
 PR 11-DEC-2000; 2000US-0251997.
 PR 05-JAN-2001; 2001US-0259678.
 (HUMA-) HUMAN GENOME SCI INC.
 PI Rosen CA, Barash SC, Ruben SM;
 PI WPI: 2001-465568/50.
 DR P-PDB: AAU19929.
 XX Isolated nucleic acid molecule encoding a calcium-binding protein is
 PT used in preventing, treating or ameliorating a medical condition -
 XX
 PS Claim 4; SEQ ID NO 48; 542pp; English.

CC The present invention relates to the isolation of novel human
 CC calcium-binding proteins (AAU1982-AAU1996), and cDNA and genomic
 CC sequences encoding for these proteins. The sequences of the invention
 CC are useful in the diagnosis, prevention and/or prognosis of diseases
 CC associated with aberrant calcium flux. Such disorders include
 CC neurological diseases (e.g. amyotrophic lateral sclerosis, ALS),
 CC immune dysfunction (e.g. severe combined immunodeficiency, SCID),
 CC digestive disorders (e.g. irritable bowel syndrome, IBS), neoplastic
 CC disease (e.g. cancer), blood disorders (e.g. hemophilia), and/or
 CC infectious disease (e.g. acquired immunodeficiency syndrome, AIDS). The
 CC novel calcium-binding proteins are also useful as screening tools to
 CC identify antagonists and/or agonists that may enhance or inhibit
 CC activities mediated by calcium-binding proteins. The polynucleotides of
 CC the invention are also useful in gene therapy. AAS31577-AAS31634
 CC represent cDNA sequences encoding for the novel human calcium-binding
 CC proteins.

CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pcl_sequences.

XX SQ Sequence 884 BP; 162 A; 273 C; 311 G; 135 T; 3 other;

Alignment Scores:
 Pred. No.: 1,71e-70 Length: 884
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US-10-031-403-1 (1-146) x AAS31614 (1-884)

PR 05-DEC-2000; 2000US-0251030.
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 PR 05-JAN-2001; 2001US-0259678.
 (HUMA-) HUMAN GENOME SCI INC.
 PI Rosen CA, Barash SC, Ruben SM;
 XX
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 DR WPI: 2001-488781/53.
 PT P-PSDB; AAM43627.
 XX
 PT
 XX
 PS Claim 1: SEQ ID NO 141; 664pp + Sequence Listing: English.
 XX
 CC The invention relates to human polynucleotides (AA163803-AA164012) and
 CC the encoded proteins (AAM434497-AAM43660) useful for preventing, treating
 CC or ameliorating medical conditions e.g. by protein or gene therapy. The
 CC genes were isolated from a range of human tissues disclosed in the
 CC specification. The nucleic acids, proteins, antibodies and (ant)agonists
 CC are useful in the diagnosis, treatment and prevention of: (a) cancer,
 CC e.g. breast and ovarian cancer and other cancers of the adrenal gland,
 CC bone, bone marrow, breast, gastrointestinal tract, liver, lung, or
 CC urogenital; (b) immune disorders e.g. Addison's disease, allergies,
 CC autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus,
 CC Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative
 CC colitis; (c) cardiovascular disorders such as myocardial ischaemia;
 CC (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and
 CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
 CC and parasitic infections.
 CC Note: The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
 CC
 XX
 SQ Sequence 884 BP; 162 A; 273 C; 311 G; 135 T; 3 other;
 Alignment Scores:
 Pred. No.: 1.71e-70 Length: 884
 Score: 722.00 Matches: 144
 Percent Similarity: 99.328 Conservative: 1
 Best Local Similarity: 98.638 Mismatches: 1
 Query Match: 99.048 Indels: 0
 DB: 22 Gaps: 0
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 Db 195 GACACGGATGAAAGCGCACCATCAATGCCCCAGAGCTGGCGCGCGCTGAGAGCCACG 254
 QY 41 GilyAsnLeuSerGluAlaGlnLeuArgLysLeuIleSerGluValAspSerAspGly 60
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 ID AAS31614 standard; cDNA; 884 BP.
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 AC AAS31614;
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 DT 04-DEC-2001 (first entry)
 XX
 DE cDNA encoding novel human calcium-binding protein #38.
 XX
 KW Human; calcium-binding protein; calcium flux; neurological disease;
 KW immune dysfunction; digestive disorder; neoplastic disease;
 KW blood disorder; infectious disease; gene therapy; immunosuppressive;
 KW antirheumatic; cytostatic; vasotropic; antibacterial; nootropic;
 KW virulence; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200153104-A2.
 XX
 PD 02-AUG-2001.
 XX
 PF 17-JAN-2001; 2001MO-US01302.
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 PR 31-JAN-2000; 2000US-0179065.
 PR 04-FEB-2000; 2000US-0180628.
 PR 24-FEB-2000; 2000US-0184664.
 PR 02-MAR-2000; 2000US-0186350.
 PR 16-MAR-2000; 2000US-0189874.
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 PR 14-AUG-2000; 2000US-0225270.
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 PR 22-AUG-2000; 2000US-0226681.
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 PR 20-OCT-2000; 2000US-0241809.
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 PR 01-DEC-2000; 2000US-0254097.
 PR 05-JAN-2001; 2001US-0259678.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Rosen CA, Barash SC, Ruben SM;
 XX
 DR WPI; 2001-581633/65.
 DR P-PDB; AAU87283.
 XX
 PT New isolated nucleic acid encoding a protein for diagnosing,
 PT preventing, treating or ameliorating medical conditions and used as
 PT food additives or preservatives -
 XX

PS Claim 1; SEQ ID No 203; 837bp; English.
 XX
 CC The invention describes an isolated nucleic acid molecule (I) encoding a
 CC novel central nervous system protein. (II) and polypeptides (III) of a
 CC by (I), are used to treat a medical conditions and in diagnosis of a
 CC pathological condition. Disorders which are diagnosed or treated include
 CC autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative
 CC disorders e.g. neoplasms of the breast or liver, cardiovascular disorders
 CC e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischemia,
 CC angiogenesis, nervous system disorders e.g. Alzheimer's disease and
 CC amyotrophic lateral sclerosis, infections caused by bacteria, viruses
 CC e.g. Acquired Immunodeficiency Virus (AIDS) and fungi, ocular disorders
 CC e.g. corneal infection, gastrointestinal disorders e.g. dysphagia,
 CC adenocarcinomas and irritable bowel syndrome, reproductive system
 CC disorders e.g. testicular feminisation, endocrine disorders e.g. diabetes
 CC and pituitary dwarfism, cancers and disorders at the cellular level e.g.
 CC leukemia, disorders involving neovascularisation e.g. malignancies,
 CC respiratory disorders e.g. nonallergic rhinitis, renal disorders e.g.
 CC acute kidney failure and blood related disorders e.g. myocardial
 CC infarction. The polypeptides can also be used to aid wound healing and
 CC epithelial cell proliferation, to prevent skin aging due to sunburn, to
 CC maintain organs before transplantation, for supporting cell culture of
 CC primary tissues, to regenerate tissues and in chemotaxis. The
 CC polypeptides can also be used as a food additive or preservative to
 CC increase or decrease storage capabilities, fat content, lipid, protein,

Alignment Scores:

Pred. No.:	6,79e-71	Length:	955
Score:	726.00	Matches:	145
Percent Similarity:	100.00%	Conservative:	1
Best Local Similarity:	99.32%	Mismatches:	0
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DB:	23	Gaps:	0

US-10-031-403-1 (1-146) x ABK43613 (1-955)

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DB	196	GACACGGATGGAACGGCACCATTAAATGCCAGAGCTGGCGCGCTGAAGCCACG	255
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 AC AA163933;

Alignment Scores:
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QY 21 AspThrAspGlyAsnGlyThrIleAsnAlaGlnGluLeuGlyAlaIleuLysAlaThr 40
|||
DB 181 GACACGATGGAAAGCCACCATCAATGCCAGAGAGTGGCCGGCGCTGAAGGCCAGC 240
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|||
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QY 61 AspGlyGluIleSerPheGlnGluPheLeuThrAlaAlaArgLysAlaArgAlaGlyLeu 80
|||
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QY 101 AspGluLeuArgAlaMetAlaGlyLeuGlyGlnProLeuProGlnGluGluLeuAsp 120
|||
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QY 141 ArgMetLeuAlaGlnGlu 146
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DB 541 AGGATCTGCGCCAGGAG 558
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AC ABK43613;
XX
XX
DT 05-JUN-2002 (first entry)
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XX
KW Central nervous system; CNS; autoimmune disease; rheumatoid arthritis;
KW hyperproliferative disorder; neoplasm; cardiovascular disorder;
KW cardiac arrest; cerebrovascular disorder; ischemia; angiodysplasia;
KW nervous system disorder; Alzheimer's disease; AIDS; ocular disorder;
KW acquired immunodeficiency virus; dysphagia; gastrointestinal disorder;
KW adenocarcinoma; reproductive system disorder; testicular feminisation;
KW endocrine disorder; diabetes; cancer; leukaemia; neovascularisation;
KW respiratory disorder; renal disorder; kidney failure; blood disorder;
KW myocardial infarction; wound healing; cell proliferation; skin aging;
KW food additive; food preservative; gene therapy; gene; ss.
OS Homo sapiens.
XX
XX
PN MO200155318-A2.
PD 02-AUG-2001.
XX
XX 17-JAN-2001; 2001MO-US01332.
XX 31-JAN-2000; 2000US-0179065.
XX 04-FEB-2000; 2000US-0180628.
PR

PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
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PR 01-SEP-2000; 2000US-0229287.
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PR 06-SEP-2000; 2000US-0230437.
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PR 29-SEP-2000; 2000US-0236327.
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PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
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 XX
 PD 26-JAN-2001.
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 XX 23-JUL-1999; 99FR-0009615.
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 XX
 XX (OREA) L'OREAL SA.
 PA Mehul B, Bernard D, Simonetti L;
 PI WPI: 2001-184569/19.
 XX P-PSDB; AAB67650.
 DR
 XX New polypeptide isolated from human skin and having calcium fixing
 PT activity, useful for regulating epidermal proliferation and
 PT differentiation, e.g. in treatment of dry skin, psoriasis or neoplasia
 PT
 PS Claim 17; Page 22; 28pp; French.
 XX
 XX The present sequence encodes a human calmodulin-like skin protein
 CC (CISP). CISP is a calcium-mediated signal pathway modulator. CISP
 CC polypeptides and polynucleotides are used cosmetically for regulating
 CC dysfunction of epidermal proliferation or differentiation (normal or
 CC pathological) and for treating dry skin, hyperkeratosis, parakeratosis,
 CC psoriasis, ichthyosis or neoplasia. They are especially used for
 CC treating skin aging and skin damage caused by exposure to ultraviolet
 CC radiation. They are also useful for preparing or purifying specific
 CC binding partners, especially specific antisera or monoclonal antibodies.
 CC
 XX
 SQ Sequence 858 BP; 155 A; 267 C; 301 G; 135 T; 0 other:
 Alignment Scores:
 Pred. No.: 2,79e-71 Length: 858
 Score: 729.00 Matches: 146
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 22 Gaps: 0
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 QY 21 AsphraspGlyasnGlyThrIleasnAlaIngluGlyAlaIleuLysAlaThr 40
 DB 174 GACACGGATGGAAACGGACCATCATATGCCAGAGGCTGGCGGCGCTTAAGGCCACG 233
 QY 41 GlyIysasnLeuSerGluAlaIngluAlaGlyLysLeuIleSerGluValAspSerAspGly 60
 DB 234 GGCAAGAACTCTCGAGAGGCCACACTAAGAACTCATCTCGAGGTTGACAGGAGCGC 293
 QY 61 AspGlyIleuIleSerPheIngluPheLeuThrAlaAlaGlyLysAlaIleuLys 80
 DB 294 GACGGCGAAACACCTTCCAGAGCTTCTGAGCGGCGGCAAGAGCGCGGCGCTG 353
 QY 81 GluAspLeuGluValAlaPheArgAlaPheAspGlnAspGlyAspGlyHisIleThrVal 100
 DB 354 GAGAACTGCGAGTCCGCTTCCGCGCTTCACAGATGGCGAGCGGCACATCACCTG 413
 QY 101 AspGluLeuArgArgAlaMetAlaGlyLeuGlyGlnProLeuProGlnGluLeuAsp 120
 DB 414 GACGAGCTCAGCGGGCGCATGCGGGGCTGGGCGAGCCGCTGCCAGAGAGACTGGAC 473
 QY 121 AlaMetIleArgGluAlaAspValAspGlnAspGlyArgValAsnTyrGluGluPheAla 140

DB 474 GCCATGATCCGCGAGCGCGAGCTGACAGACGGGGGTGAACACTAGAGAGACTCGC 533
 QY 141 ArgMetLeuAlaInglu 146
 DB 534 AGGATGCTCGGCCACGAG 551
 RESULT 2
 ID AAA10473 standard; cDNA; 853 BP.
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 AC AAA10473;
 XX
 DT 18-JUL-2000 (first entry)
 XX
 DE cDNA encoding human disease-associated calmodulin protein (DACP-1).
 XX
 KW Disease-associated calmodulin protein; DACP-1; human; EF-hand;
 KW detection; quantitation; diagnosis; cancer; immune disorder;
 KW reproductive disorder; gynaecological; gene therapy; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 121..561
 FT /*tag= a
 FT /product= "Human DACP-1"
 PN US6046315-A.
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 PD 04-APR-2000.
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 XX 03-NOV-1997; 97US-0963409.
 PF 03-NOV-1997; 97US-0963409.
 XX
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 PR
 PA (INCYTE) INCYTE PHARM INC.
 XX
 PI Hillman J, Corley NC, Shah P;
 XX
 XX WPI: 2000-282708/24.
 DR P-PSDB; AAB67548.
 XX
 XX New polynucleotide encoding a disease associated calmodulin protein
 PT (DACP-1) useful for diagnosing, preventing and treating cancer. Immune
 PT disorders and reproductive disorders
 PT
 PS Claim 4; Fig 1A-C; 27pp; English.
 XX
 XX This sequence represents cDNA encoding human disease-associated
 CC calmodulin protein (DACP-1). cDNA sequences encoding DACP-1 were
 CC initially isolated from a breast tumour cDNA library, this sequence
 CC being a consensus. Human DACP-1 has four EF-hand calcium-binding
 CC domains, and has chemical and structural homology with other calmodulin
 CC proteins from human, rat and Plasmodium falciparum. DACP-1 proteins and
 CC nucleotides are useful for the diagnosis, prevention, or treatment of
 CC cancers, immune disorders (e.g., AIDS) and reproductive disorders,
 CC including endometriosis. DACP-1 nucleotides are useful for detecting and
 CC quantitating gene expression in biopsied tissues in which expression of
 CC the protein may be correlated with a disease. Such a diagnostic assay may
 CC be used to distinguish between absence, presence, and overexpression of
 CC DACP-1, and to monitor regulation of DACP-1 levels during therapeutic
 CC intervention. The nucleotide sequences are also useful in assays used to
 CC evaluate the efficacy of a particular therapeutic treatment regimen in
 CC animal studies, in clinical trials, or in monitoring the treatment of an
 CC individual patient. Nucleotides encoding DACP-1 are also useful in
 CC modulating DACP-1 expression e.g., in antisense therapy. DACP-1, and
 CC DACP-1 fragments and antibodies may be used in drug screening techniques.
 CC The antibodies may also be useful for the diagnosis of diseases
 CC associated with abnormal DACP-1 expression or activity.
 XX
 SQ Sequence 853 BP; 150 A; 270 C; 303 G; 130 T; 0 other;

GenCore version 5.1.4-p5.4578
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OM protein - nucleic search, using frame_plus_p2n model

Run on: May 16, 2003, 02:34:02 ; Search time 243 Seconds

(without alignments)
1353.052 Million cell updates/sec

Title: US-10-031-403-1

Perfect score: 729
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Scoring table:

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Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
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Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
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3	726	99.6	955	23	ABK43613	Human encoding nove
4	722	99.0	884	22	AAI63933	Human polynucleoti
5	722	99.0	884	22	AAI63933	cDNA encoding nove
6	722	99.0	884	22	ABK43908	DNA encoding novel
7	722	99.0	884	22	AAI63855	Human polynucleoti
8	529	72.6	497	21	AAE21853	Human breast and o
9	384.5	52.7	447	11	AAO04331	Recombinant calmod
10	384.5	52.7	450	16	AAO95549	Human calmodulin c
11	384.5	52.7	485	24	ABK44905	cDNA encoding colo
12	384.5	52.7	504	11	AAO04334	Plasmid pOCAL7 con
13	384.5	52.7	564	21	AAO03838	Human secreted pro
14	384.5	52.7	654	11	AAO04332	Plasmid pRCM1 and
15	384.5	52.7	654	24	ABK63445	Rat sequence diffe
16	384.5	52.7	1131	11	AAO05826	Human calmodulin g
17	384.5	52.7	1361	24	ABI99274	Mouse ischaemic co
18	384.5	52.7	2175	24	ABK83767	Human cDNA differe
19	384.5	52.7	2247	22	AAI44950	cDNA encoding nove
20	380.5	52.2	739	23	ABL20145	Drosophila melanog
21	380.5	52.2	995	23	ABL14119	Drosophila melanog
22	380.5	52.2	1049	23	ABL20141	GST-calmodulin fus
23	380.5	52.2	1128	16	AAO95552	Rat calmodulin enc
24	379.5	52.1	447	24	ABN83905	Protein A-calmodul
25	379.5	52.1	1230	16	AAO95551	Calcium binding pr
26	379.5	52.1	1608	16	AAO95550	Calcium sensor G85
27	376.5	51.6	1251	24	ABN83907	Fluorescent calmod
28	376.5	51.6	1929	19	AAV58275	Fluorescent calmod
29	376.5	51.6	1958	19	AAV58276	Fluorescent calmod
30	373.5	51.2	1929	19	AAV58277	Fluorescent calmod
31	373.5	51.2	1929	19	AAV58278	Human ovarian PC
32	371.5	51.0	624	22	AAI25303	Human ovarian PC
33	371.5	51.0	624	22	AAI25303	Human ovarian PC
34	371.5	51.0	624	22	AAH82499	Human ovarian PC
35	370.5	50.8	462	9	AAH80188	DNA encoding biosy
36	358.5	49.2	681	21	AAI10892	Human secreted pro
37	357.5	49.0	1306	24	ABL65422	Lung cancer relate
38	357.5	49.0	1306	24	ABL65422	Lung cancer relate
39	357.5	49.0	1306	24	ABL67798	Oesophagus cancer
40	357.5	49.0	2746	24	ABL67803	Oesophagus cancer
41	355.5	48.8	672	24	ABO65821	Arabidopsis thalia
42	355.5	48.8	751	21	AAI33827	Arabidopsis thalia
43	355.5	48.8	906	17	AAI18078	Potato calmodulin
44	355.5	48.8	1133	20	AAI27544	Human ovarian tumo
45	352.5	48.4	456	21	AAI49319	Arabidopsis thalia

ALIGNMENTS

RESULT 1
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AAE55621 standard; DNA; 858 BP.

29-MAY-2001 (first entry)

Nucleotide sequence of a human calmodulin-like skin protein.

Human; calmodulin-like skin protein; CLSF; epidermal differentiation;

calcium-mediated signal pathway; epidermal proliferation; dry skin;

hyperkeratosis; parakeratosis; psoriasis; ichthyosis; neoplasia;

skin aging; skin damage; ss.

Homo sapiens.

Location/Qualifiers

Alignment Scores:

Pred. No.:	1,08e-22	Length:	654
Score:	384.50	Matches:	76
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Query Match:	52.74%	Indels:	3
DB:	6	Gaps:	2

US-10-031-403-1 (1-146) x E02315 (1-654)

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DB 172 GATTAAGATGGGACGGACCATCAACAAGAGAGCTGGGACTGCTCATGCGGTCACGTG 231
    ||| ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
OY 41 GlyLysAsnLeuSerGluAlaGlnLeuArgLysLeuIleSerGluValAspSerAspGly 60
    ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
DB 232 GGTCAAGAACCCACAGAGAGCTGACTGCGATATGATCAACGAGGTGATGCCAGCGG 291
    ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
OY 61 AspGlyGluIleSerPheGlnGluPheLeuThr---AlaAlaArgLysAlaArg----- 77
    :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
DB 292 AATGCACCATGACTGCCAGAGCTTCTGACTATGATGCTAAGAAAATGAAGACACA 351
    :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
OY 78 AlaGlyLeuGluAspLeuGlnValAlaPheArgAlaPheAspGluAspGlyHis 97
    ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
DB 352 GATACCGAAGAAATCGGTAGGCAATCCAGTCTTGGACAGAGATGGCAATGGCTTAC 411
    ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
OY 98 IleThrValAspGluLeuArgAlaMetAlaGlyLeuGlnProLeuProGlnGlu 117
    ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
DB 412 ATCAGTGGGGCGAGACTGGCCACGTCATGACAAACCTCGGGAAAGCTAACAGATGAA 471
    ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
OY 118 GluLeuAspAlaMetIleArgGluAlaAspValAspGluAspGlyArgValAsnTyrGlu 137
    ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
DB 472 GAAGTAGACGAATGATCAGAGAACGCAATATTGATGAGACGACAGCTCAACTATGAA 531
    ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
OY 138 GluPheAlaArgMetLeu 143
    ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
DB 532 GAATTCGTACAGATGATG 549
    ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||

```

Search completed: May 16, 2003, 04:30:11
 Job time : 2517 secs

US-10-031-403-1 (1-146) x AY046946 (1-622)

QY 1 MetAlaGlyGluLeuThrProGluGluAlaGlnGlyTyrLysAlaPheSerAlaVal 20
 DB 69 ATGGCTGACCAAGCTGACAGAGATTGCAAAATTCAGAACCTTTTCATATTT 128
 QY 21 AspThrAspGlyAsnGlyThrIleAsnAlaGlnGluLeuGlyAlaIleLeuLysAlaThr 40
 DB 129 GACAAAGATGGTGTAGTAATACAAACAAGAAATTTGGAGACTGTAATGCGGTCTT 188
 QY 41 GlyLysAsnLeuSerGluAlaGlnLeuArgLysLeuIleSerGluValAspSerAspGly 60
 DB 189 GGGCAACATCCCAAGACAGAGATTACAGGACATGATTAATGAGTAGATGCTGATGTT 248
 QY 61 AspGlyGluIleSerPheGlnGluPheLeuThr---AlaIleArgLysAlaArg----- 77
 DB 249 AATGGCAACATTAATTCCTCCGAAATTTCTGACATGATGCAAGAAATGAAAGATACA 308
 QY 78 AlaGlyLeuGluAspLeuGlnValAlaPheArgAlaPheAspGlnAspGlyAspGlyHis 97
 DB 309 GACAGTGAAGAAAGAAATTAAGAGAACATTCCTGTTGATTAAGATGTAATGGCTAT 368
 QY 98 IleThrValAspGluLeuArgArgAlaMetAlaGlyLeuGlnProLeuProGlnGlu 117
 DB 369 AATAGTGCAGCAGACAGCTCCGCTGATGATGACAAACCTTGAGAGAACTTAACAGATGAA 428
 QY 118 GluLeuAspAlaMetIleArgGluAlaAspValAspGlnAspGlyArgValAsnTyrGlu 137
 DB 429 GAGCTTGATCAATGATCAAGGAGACAGATTTGATGATGCTCAAGTAACTATGAA 488

QY 138 GluPheAlaArgMetLeu 143
 DB 489 GAGTTGTACAAATGATG 506

RESULT 14
 AX401676 654 bp DNA linear PAT 06-JUN-2002
 LOCUS AX401676
 DEFINITION Sequence 1352 from Patent WO0210453.
 ACCESSION AX401676
 VERSION AX401676.1 GI:21337856
 KEYWORDS

SOURCE Norway rat.
 ORGANISM Rattus norvegicus

REFERENCE 1
 AUTHORS Mendrick,D., Porter,M.W., Johnson,K.R., Castle,A.L. and
 TITLE Elashoff,M.R.
 JOURNAL Molecular toxicology modeling.
 Patent: WO 0210453-A 1352 07-FEB-2002;
 Gene Logic, Inc. (US)
 Rattus.
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

FEATURES
 source 1..654
 /organism="Rattus norvegicus"
 /db_xref="taxon:10116"
 /note="EMBL/GenBank Accession No. E02315"

BASE COUNT 214 a 153 c 159 g 128 t
 ORIGIN

Alignment Scores:

Pred. No.: 1.08e-22 Length: 654
 Score: 384.50 Matches: 76
 Percent Similarity: 73.97% Conservative: 35
 Best Local Similarity: 52.05% Mismatches: 35
 Query Match: 52.74% Indels: 3
 DB: 6 Gaps: 2

US-10-031-403-1 (1-146) x AX401676 (1-654)

QY 1 MetAlaGlyGluLeuThrProGluGluAlaGlnGlyTyrLysAlaPheSerAlaVal 20
 DB 69 ATGGCTGACCAAGCTGACAGATTGCAAAATTCAGAACCTTTTCATATTT

DB 112 ATGGCTGATCAGCTGACGAGAACAGATTGCTGAATTCAGAACCTTTCTCCATATTT 171

QY 21 AspThrAspGlyAsnGlyThrIleAsnAlaGlnGluLeuGlyAlaIleLeuLysAlaThr 40
 DB 172 GATTAAGATGGGACGCGACATCATCAACAAGAGCTGGGAGCTGTCAATGCGGTCACTG 231

QY 41 GlyLysAsnLeuSerGluAlaGlnLeuArgLysLeuIleSerGluValAspSerAspGly 60
 DB 232 GGTCAAGAACCAACAGAGCTGAATGACGATATGATCAACAGAGTGTGCTCGCAGCGG 291

QY 61 AspGlyGluIleSerPheGlnGluPheLeuThr---AlaIleArgLysAlaArg----- 77
 DB 292 AATGGCAACCTTAATTCCTCCGAAATTTCTGACATGATGCTGAAATGAAAGACACA 351

QY 78 AlaGlyLeuGluAspLeuGlnValAlaPheArgAlaPheAspGlnAspGlyAspGlyHis 97
 DB 352 GATAGCAAGAACAAATTCCTGAGCGATTCGAGATCTTTGACAAAGATGGCATGGCTAC 411

QY 98 IleThrValAspGluLeuArgArgAlaMetAlaGlyLeuGlnProLeuProGlnGlu 117
 DB 412 ATCAGTCCGCGCAGACAGCTCCGCTGATGATGACAAACCTCGGGAAGAACTTAACAGATGAA 471

QY 118 GluLeuAspAlaMetIleArgGluAlaAspValAspGlnAspGlyArgValAsnTyrGlu 137
 DB 472 GAGTGTGACAAATGATCAAGAGACAGATTTGATGAGACGACAGCTCAACTATGAA 531

QY 138 GluPheAlaArgMetLeu 143
 DB 532 GAATTCGTACAGATGATG 549

RESULT 15
 E02315 654 bp RNA linear PAT 29-SEP-1997
 LOCUS E02315
 DEFINITION DNA encoding calmodulin.
 ACCESSION E02315
 VERSION E02315.1 GI:2170551
 KEYWORDS JP 1990092286-A/2.
 SOURCE Rattus norvegicus.
 ORGANISM Rattus norvegicus
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.
 1 (bases 1 to 654)
 AUTHORS Ozawa,T., Matsuki,S. and Nozawa,Y.
 TITLE PRODUCTION OF CALMODULIN
 JOURNAL Patent: JP 1990092286-A 2 03-APR-1990;
 KIRIN BREWERY CO LTD
 OS Rat

COMMENT 1 (bases 1 to 654)
 PN JP 1990092286-A/2
 PD 03-APR-1990
 PF 30-SEP-1988 JP 1988246239
 PI OZAWA TADASHI, MATSUKI SHIGERU, NOZAWA YOSHINORI PC
 C12N15/12,C07H21/04,C07K13/00,C12P21/02,C12P21/02,C12R1:19); CC
 strandedness: Double;
 CC topology: Linear;
 CC hypothetical: No;
 CC anti-sense: No;
 CC *source: clone-PRCM1;
 CC Feature is identified by experimental;
 FH key Location/Qualifiers

FEATURES
 source 1..654
 /organism="Rattus norvegicus"
 /db_xref="taxon:10116"

FT 5'UTR 1..111
 FT CDS 112..561
 FT mat_peptide /product="calmodulin"
 FT 112..558
 FT /product="calmodulin"
 FT 562..654.
 FT 3'UTR Location/Qualifiers

BASE COUNT 214 a 153 c 159 g 128 t
 ORIGIN

Db 266 GGTCAAGACCCGACAGAGCTGAGCTCCAGACATGATCAACAGAGCTGCATCCGATGCA 325
 Oy 61 AspglygluileserPhegInglupheleuthr---AlaAlaArgLysAlaArg----- 77
 Db 326 AATGGACCATGATTTCCAGAGTCTCTCAGCATGATGCGCAGAGATGAAGACAGC 385
 Oy 78 AlaGlyLeuGluAspLeuGlnValAlaPheArgAlaPheAspGlnAspGlyAspGlyHis 97
 Db 386 GACACGGAAGAGAGATGAGGAGACGCTTCAGAGCTTTGACAGAGATGCAACGCGCTAC 445
 Oy 98 IleThrValAspGluLeuArgArgAlaMetAlaGlyLeuGlnProleuprogInglu 117
 Db 446 ATCAGCGCTGCTGAGCTGACGTGAGAGAAATCTCGCGAGAACTGACAGACGAG 505
 Oy 118 GluLeuAspAlaMetIleArgGlnAlaAspValAspGlnAspGlyArgValAsnArgIu 137
 Db 506 GAGGTGAGCAATATGATCAGGAGACCCAGCATCGATGCGAGAGCTCAACTATGAA 565
 Oy 138 GluPheAlaArgMetLeu 143
 Db 566 GAATTTGTGCAATGATG 583

RESULT 12

LOCUS RATCMB 599 bp mRNA linear ROD 27-APR-1993
 DEFINITION Rat calmodulin mRNA, complete cds, clone pRCM79.
 ACCESSION M16659
 VERSION M16659.1 GI:203259
 KEYWORDS calmodulin.
 SOURCE Rat (strain Sprague-Dawley) male brain, cDNA to mRNA, clone pRCM79.
 ORGANISM Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.

REFERENCE 1 (bases 1 to 599)
 AUTHORS Sherbany, A.A., Parent, A.S. and Brosius, J.
 TITLE Rat calmodulin cDNA
 JOURNAL DNA 6 (3), 267-272 (1987)
 MEDLINE 87246077
 PUBMED 2885164

FEATURES

source
 1..599 Location/Qualifiers
 /organism="Rattus norvegicus"
 /db_xref="taxon:10116"
 <1..599
 /product="calmodulin mRNA"
 11..460
 /note="calmodulin"
 /codon_start=1
 /protein_id="AAA40864.1"
 /db_xref="GI:203260"
 /translation="MADOLTEEQIAEFKFAFLSPDKDGGTITTKELGTVMKSLGONP
 TEAELODMINEVDADNGTIDPEFLTVMARKMDTDEEELREAFRFDDNGNYS
 AAELRHVNTNGEKLTDEVDENIREADIDGQVNYEEFQVMYAK"

BASE COUNT 158 a 140 c 176 g 125 t
 ORIGIN 9 bp upstream of NcoI site.

Alignment Scores:

Pred. No.: 9.87e-23 Length: 599
 Score: 384.50 Matches: 76
 Percent Similarity: 73.97% Conservative: 32
 Best Local Similarity: 52.05% Mismatches: 35
 Query Match: 52.74% Indels: 3
 Gaps: 2

US-10-031-403-1 (1-146) x RATCMB (1-599)

Oy 1 MetAlaGlyLeuLeuThrProGluGluGluAlaGlnIleValLysAlaPheSerAlaVal 20
 Db 11 ATGGGTGACGACGATGACGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAG 70
 Oy 21 AsprhAspGlyAsnGlyThrIleAsnAlaGlnGluLeuGlyAlaAlaLeuLysAlaThr 40

Db 71 GACAGAGATGAGATGACCATTCACCAAGAGAGCTGATGATGATGCTG 130
 Oy 41 GlyLysAsnLeuSerGlnAlaGlnLeuArgLysIleSerGluValAspSerAspGly 60
 Db 131 GGGCAAAACCCACACACGCGGAGACTGCGACATCATCATCATCATCATCATCATCAT 190
 Oy 61 AspglygluileserPhegInglupheleuthr---AlaAlaArgLysAlaArg----- 77
 Db 191 AATGGACCATGATGATTCCTCCAGAGTCTCGACCATGATGCGCAGAAAGATGAGATGCA 250
 Oy 78 AlaGlyLeuGluAspLeuGlnValAlaPheArgAlaPheAspGlnAspGlyAspGlyHis 97
 Db 251 GACACGAGAGAGATGAGATGAGAGAGCTTCGCTTTGACAGAGATGGAATGCTTAC 310
 Oy 98 IleThrValAspGluLeuArgArgAlaMetAlaGlyLeuGlnProleuprogInglu 117
 Db 311 ATCAGTGTCTGAGCTGCTGCTCAGCATGACAGACCTGGGAGAGACTGACTGATGAG 370
 Oy 118 GluLeuAspAlaMetIleArgGlnAlaAspValAspGlnAspGlyArgValAsnArgIu 137
 Db 371 GAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 430
 Oy 138 GluPheAlaArgMetLeu 143
 Db 431 GAGTTTGTACAGATGATG 448

RESULT 13

LOCUS AY046946 622 bp mRNA linear MM 18-SEP-2001
 DEFINITION Ovis aries calmodulin 2 (CALM2) mRNA, complete cds.
 ACCESSION AY046946
 VERSION AY046946.1 GI:15667248
 KEYWORDS
 SOURCE Ovis aries.
 ORGANISM Ovis aries
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 Bovidae; Caprinae; Ovis.

REFERENCE 1 (bases 1 to 622)
 AUTHORS Gillett, A.M., Wallace, M.J., Gillespie, M.T. and Hooper, S.B.
 TITLE Increased expansion of the lung stimulates calmodulin 2 expression in fetal sheep
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 622)
 AUTHORS Gillett, A.M., Wallace, M.J., Gillespie, M.T. and Hooper, S.B.
 TITLE Direct submission
 JOURNAL Submitted (19-JUL-2001) Physiology Dept., Monash University, Wellington Rd, Clayton, Vic 3800, Australia

FEATURES

source
 1..622 Location/Qualifiers
 /organism="Ovis aries"
 /db_xref="taxon:9940"
 1..622
 /gene="CALM2"
 69..518
 /gene="CALM2"
 /codon_start=1
 /product="calmodulin 2"
 /protein_id="AAL02363.1"
 /db_xref="GI:15667249"
 /translation="MADOLTEEQIAEFKFAFLSPDKDGGTITTKELGTVMKSLGONP
 TEAELODMINEVDADNGTIDPEFLTVMARKMDTDEEELREAFRFDDNGNYS
 AAELRHVNTNGEKLTDEVDENIREADIDGQVNYEEFQVMYAK"

BASE COUNT 206 a 93 c 161 g 162 t
 ORIGIN

Alignment Scores:

Pred. No.: 1.03e-22 Length: 622
 Score: 384.50 Matches: 76
 Percent Similarity: 73.97% Conservative: 32
 Best Local Similarity: 52.05% Mismatches: 35
 Query Match: 52.74% Indels: 3
 Gaps: 2

QY 41 GlyLysAsnLeuSerGluAlaGlnLeuArgLysLeuIleSerGluValAspSerAspGly 60
 DB 121 GGTCAAAATCCACAGAGCAATGACGATGATCAACAGAGATGCTGATGCG 180
 QY 61 AspGlyGluIleSerPheGlnGluPheLeuThr---AlaAlaArgLysAlaArg----- 77
 DB 181 AATGGCACTATCAGCTTCTGTAATCTTAAACATGATGCGCAGAAAATGAAGGACACA 240
 QY 78 AlaGlyLeuGlnLysAspGlnValAlaPheArgAlaPheAspGlnAspGlyAspGlyHis 97
 DB 241 GACAGGAGAGAAATCCCTGAGCGATTCGAGTCTTTACAGATGCGCAATGCTTAT 300
 QY 98 IleThrValAspGluLeuArgArgAlaMetAlaGlyLeuGlnGlnProLeuProGlnGlu 117
 DB 301 ATCAGTGGCGCAGAGCTACGTCATGTTATGACAACTAGAGAAAAGCTAACAGATGAA 360
 QY 118 GluLeuAspAlaMetIleArgGluAlaAspValAspGlnAspGlyArgValAsnTyrglu 137
 DB 361 GAAGTAGACAAATGATCAAGAGACAGACATGATGGGATGGGCAAGTCAACTATGAA 420
 QY 138 GluPheAlaArgMetLeu 143
 DB 421 GAATTCGTACAGATGATG 438

RESULT 10 AX396241 485 bp DNA 1linear PAT 18-MAY-2002
 LOCUS AX396241 Sequence 456 from Patent WO0212328.
 DEFINITION AX396241
 ACCESSION AX396241
 VERSION AX396241.1 GI:21066988
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE 1
 AUTHORS King, G. E., Meagher, M. J., Xu, J. and Secrist, H.
 TITLE Compositions and methods for the therapy and diagnosis of colon cancer
 JOURNAL Patent: WO 0212328-A 456 14-FEB-2002;
 CORIXA CORPORATION (US)
 FEATURES
 source Location/Qualifiers
 1..485
 /organism="Homo sapiens"
 /db_xref="taxon:9606"

BASE COUNT 168 a 69 c 130 g 118 t
 ORIGIN

Alignment Scores:
 Pred. No.: 7.9e-23 Length: 485
 Score: 384.50 Matches: 76
 Percent Similarity: 73.97% Conservative: 32
 Best Local Similarity: 52.05% Mismatches: 35
 Query Match: 52.74% Indels: 3
 DB: 6 Gaps: 2

US-10-031-403-1 (1-146) x AX396241 (1-485)

QY 1 MetAlaGlyLeuLeuThrProGlnGluAlaGlnIleTyrgLysAlaPheSerAlaVal 20
 DB 44 ATGGCGACCACTGACGAGAGAGATGCGAATTCAGAAAGCTTTTTCACATTT 103
 QY 21 AspThrAspGlyAsnGlyThrIleAsnAlaGlnGluLeuGlyAlaAlaLeuLysAlaThr 40
 DB 104 GACAAAGATGCTGATGATTAACAAACAAAGAAATTTGGAACTGTAAAGATCTCTT 163
 QY 41 GlyLysAsnLeuSerGluAlaGlnLeuArgLysLeuIleSerGluValAspSerAspGly 60
 DB 164 GGGCAGATCCACAGAGAGAGATGACAGACATGATTAATAGTAGATGCTGATGT 223
 QY 61 AspGlyGluIleSerPheGlnGluPheLeuThr---AlaAlaArgLysAlaArg----- 77
 DB 224 AATGGCACTATGCTTCCCTGAAATTTCTGACATGATGCGCAAGAAAAGAGACACA 283

QY 78 AlaGlyLeuGlnLysAspGlnValAlaPheArgAlaPheAspGlnAspGlyAspGlyHis 97
 DB 284 GACAGTGAACAAATTAAGAGACATTCGCTGTTTATAGAGATGCGCAATGCTAT 343
 QY 98 IleThrValAspGluLeuArgArgAlaMetAlaGlyLeuGlnGlnProLeuProGlnGlu 117
 DB 344 ATTAGTCTCAGCAACTCCCATGTCATGACCAACCTTGAGAGAACTTAACAGATGAA 403
 QY 118 GluLeuAspAlaMetIleArgGluAlaAspValAspGlnAspGlyArgValAsnTyrglu 137
 DB 404 GAAGTTGATGAATGATCAAGAGAGAGATATGATGATGTCATCAAGTAACTATGAA 463
 QY 138 GluPheAlaArgMetLeu 143
 DB 464 GAGTTTGTACAAATGATG 481

RESULT 11 SYNARBCAL 595 bp mRNA 1linear SYN 27-APR-1993
 LOCUS SYNARBCAL A.punctulata synthetic calmodulin mRNA, complete cds.
 DEFINITION 104729
 ACCESSION 104729
 VERSION 104729.1 GI:207976
 KEYWORDS calmodulin.
 SOURCE A.punctulata (adult), cDNA to mRNA, clone M13MP18.
 ORGANISM artificial construct
 1 (bases 1 to 595)
 AUTHORS Persechini, A., Blumenthal, D. K., Jarrett, H. W., Klee, C. B., Hardy, D. O.
 and Kreislinger, R. H.
 TITLE The effects of deletions in the central helix of calmodulin on enzyme activation and peptide binding
 JOURNAL J. Biol. Chem. 264 (14), 8052-8058 (1989)
 MEDLINE 89255236
 PUBMED 2542260
 COMMENT A.a. entry and computer-readable sequence for [1] kindly provided by A.J. Persechini, 17-FEB-1989.
 FEATURES
 source Location/Qualifiers
 1..595
 /organism="synthetic construct"
 /db_xref="taxon:32630"
 146..595
 /note="calmodulin"
 /codon_start=1
 /transl_table=11
 /protein_id="AA072214.1"
 /db_xref="GI:207976"
 /translation="MADQLTEBOIAEFKRAFSLPDKDGGCTTTKEIGVMSIGONP
 TENELQDMINEVDADNGTIDPEPFLTMARKKDKDSEETREARFVFDKQNGTIS
 AAELEKRVMTNIEKLTDEEVDKIRADIDGQVNYEEFVQMTRAK"

BASE COUNT 172 a 142 c 164 g 117 t
 ORIGIN

Alignment Scores:
 Pred. No.: 9.8e-23 Length: 595
 Score: 384.50 Matches: 76
 Percent Similarity: 73.97% Conservative: 32
 Best Local Similarity: 52.05% Mismatches: 35
 Query Match: 52.74% Indels: 3
 DB: 12 Gaps: 2

US-10-031-403-1 (1-146) x SYNARBCAL (1-595)

QY 1 MetAlaGlyLeuLeuThrProGlnGluAlaGlnIleTyrgLysAlaPheSerAlaVal 20
 DB 146 ATGGCTGACCACTACACGAGAGAGATGCGAATTCAGAAAGCTTTCTCCCTGTC 205
 QY 21 AspThrAspGlyAsnGlyThrIleAsnAlaGlnGluLeuGlyAlaAlaLeuLysAlaThr 40
 DB 206 GACAAAGAGCGGATGCGCAACATCAACCAAGAGAGCTGGGACCGTGAATGATCTCTT 265
 QY 41 GlyLysAsnLeuSerGluAlaGlnLeuArgLysLeuIleSerGluValAspSerAspGly 60

Oy	98	IlethrValaspGluLeuArGarglaIleMetAlaGlyLysGlnProLeuProGlnGlu	117
Dd	301	ATTACTGCTGCAGCACTTCGCCATGTGATGACAAACCCTTGCGAGACAAGTTAACAGATGCA	360
Oy	118	GluLeuAspAlaMeTlleArgGluAlaLaaspAlaSpGlnAspGlyArgValAsnTryGlu	137
Dd	361	GAAGTGTATGAATAATGATCAGGAGACGACAGATATTGATGGTAGTCAAGTAACATATGAA	420
Oy	138	GluPheAlaArgMetLeu	143
Dd	421	GAGTTTGTACAAATGATG	438
RESULT	9		
LOCUS	DUKCA	476 bp	mRNA linear VRT 30-JUL-1999
DEFINITION	Anas platyrhynchos mRNA for calmodulin, complete cds.		
ACCESSION	D83350		
VERSION	D83350.1	GI:1199918	
KEYWORDS	calmodulin.		
SOURCE	Anas platyrhynchos cDNA to mRNA, clone_11b:lambda ZAP II clone.pDI-34.		
ORGANISM	Anas platyrhynchos		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Anseriformes; Anatidae; Anas.		
AUTHORS	Kimura,N., Kurosawa,N., Kondo,K. and Tsukada,Y.		
TITLE	Molecular cloning of the kainate-binding protein and calmodulin genes which are induced by an imprinting stimulus in ducklings		
JOURNAL	Brain Res. Mol. Brain Res. 17 (3-4), 351-355 (1993)		
MEDLINE	93487810		
REFERENCE	2 (bases 1 to 476)		
AUTHORS	Kimura,N.		
TITLE	Direct Submission		
JOURNAL	Submitted (05-FEB-1996) Naohiro Kimura, Soka University, Dept. of Bioengineering, Faculty of Engineering; 1-236 Tangicho, Hachioji, Tokyo 192, Japan (E-mail:kimura@ccl.t.soka.ac.jp, Tel:0426-91-9442, Fax:0426-91-9312)		
FEATURES	location/Qualifiers		
SOURCE	1..476		
	/organism="Anas platyrhynchos"		
	/db_xref="taxon:8839"		
	/clone="pDI-34"		
	/clone_11b="lambda ZAP II"		
CDS	1..450		
	/codon_start=1		
	/product="calmodulin"		
	/protein_id="BAAL1896.1"		
	/db_xref="GI:1199919"		
	/translation="MADOLTEEOIAEFKEAFSLFDKDGDGITTKRELGYVRSIGONPR TEALQDMINEVDAGNGITDPEFLFMARKNMDTSEEEIRAFYFIDKGNGYIS AALRHWTNIGEKLTDEVEDEMIREADIDGDGVNVEEFQWMTAK"		
BASE COUNT	162 a 84 c 122 g 108 t		
ORIGIN			
Alignment Scores:			
Pred. NO.:	7.75e-23	Length:	476
Score:	384.50	Matches:	76
Percent Similarity:	73.97%	Conservative:	32
Best Local Similarity:	52.05%	Mismatches:	35
Query Match:	52.74%	Indels:	3
DB:	5	Gaps:	2
US-10-031-403-1 (1-146) x DUKCA (1-476)			
Oy	1	MetaLaGlyGluLeuThrPrroGluGluGluAlaGlnTrfYfsLYsAlaPhseSerAlaVal	20
Dd	1	ATGGCTGATCAACHTGACGAAGACAGATGTCTGAGTTCAAGGAAGCCCTTTCCCTATT	60
Oy	21	AsprThAspsGlyAsnGlyThrIleLsnAlaGlnGluGluGlyAlaAlaLeuLysLatThr	40
Dd	61	GACACGAGGTGGTGTGATGTACTATCACAAACAAGAAGTGGGAAGTGTATGATGAGGCGTTG	120

REFERENCE 1 (bases 1 to 447)
 AUTHORS Ozawa, T., Matsuki, S. and Nozawa, Y.
 TITLE PRODUCTION OF CALMODULIN
 JOURNAL Patent: JP 1990092286-A 1 03-APR-1990;
 KIRIN BREWERY CO LTD

COMMENT

OS Rat
 PN JP 1990092286-A/1
 PD 03-APR-1990
 PF 30-SEP-1988 JP 1988246239
 PT OZAWA TADASHI, MATSUKI SHIGERU, NOZAWA YOSHINOBU PC
 C12N15/12,C07H21/04,C07K13/00,C12P21/02,C12P21/02,C12R1:19); CC
 strandedness: Double;
 CC topology: Linear;
 CC hypothetical: No;
 CC anti-sense: No;
 CC *source: clone-PTCAL7;
 CC Feature is identified by experimental;
 FH Key Location/Qualifiers

FEATURES
 source location/Qualifiers
 1..447
 /organism="Rattus norvegicus"
 /db_xref="taxon:10116"

BASE COUNT 155 a 87 c 122 g 83 t
 ORIGIN

Alignment Scores:

Pred. No.: 7.25e-23 Length: 447
 Score: 384.50 Matches: 76
 Percent Similarity: 73.97% Conservative: 32
 Best Local Similarity: 52.05% Mismatches: 35
 Query Match: 52.74% Indels: 3
 DB: 6 Gaps: 2

US-10-031-403-1 (1-146) x E02314 (1-447)

QY 1 MetAlaGlyLeuThrProGluGluGluAlaGlnTyrLysLysAlaPheSerAlaVal 20
 Db 1 ATGGCAGATCAATTAACAGAGAAAGATGCGTAATTCAGAAAGAGCTTTCTCCCTATT 60
 QY 21 AspThrAspGlyAsnGlyThrIleAsnAlaGlnGluLeuGlyAlaAlaLeuLysAlaThr 40
 Db 61 GATTAAGATGGGAGCGGACCATCACAACAAGAGAGCTGGGACTGTCATCGCTCACTG 120
 QY 41 GlyLysAsnLeuSerGluAlaGlnLeuArgLysLeuIleSerGluValAspSerAspGly 60
 Db 121 GGTGACAGAACCCACAGAGCTGTAATCTGACAGATTCATCAACGAGTGATGCCGACGG 180
 QY 61 AspGlyLeuIleSerPheGlnGluPheLeuThr---AlaAlaArgLysAlaArg----- 77
 Db 181 AATGGGACCCATGCTCCAGAGTCTCTGATGATGCTAGAAAAAATGAAGAAACACACA 240
 QY 78 AlaGlyLeuGluAspLeuGlnValAlaPheArgAlaPheAspGlnAspGlyAspGlyHis 97
 Db 241 GATAGCGAAGAAGAAATCCGTAGCGCATTCGAGCTCTTGCACAAGATGGCAATGCGTAC 300
 QY 98 IleThrValAspGluLeuArgArgAlaMetAlaGlyLeuGlnProLeuProGlnGlu 117
 Db 301 ATGAGTCCGCGACAAAGCCGACGTCATGACAAACCTCGGGGAAAGCTTAACAGATGAA 360
 QY 118 GluLeuAspAlaMetIleArgGluAlaAspValAspGlnAspGlyArgValAspTyrGlu 137
 Db 361 GAAGTACACAAATGATCAGAGAGAGATATGATGAGAGCGACGCTCAACTATGAA 420
 QY 138 GluPheAlaArgMetLeu 143
 Db 421 GAATTCCTACAGATGATG 438

RESULT 7
 CHKCALMA 450 bp mRNA linear VRT 28-APR-1993
 LOCUS Chicken calmodulin mRNA, complete cds.
 DEFINITION M36167.1 GI:211385
 ACCESSION M36167.1 GI:211385
 VERSION
 KEYWORDS Chicken, cDNA to mRNA.
 SOURCE Gallus gallus
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;

REFERENCE 1 (bases 1 to 450)
 AUTHORS Iida, Y.
 TITLE cDNA sequences and molecular evolution of calmodulin genes of chicken and eel

JOURNAL Bull. Chem. Soc. Jpn. 57, 2667-2668 (1984)
 FEATURES location/Qualifiers

source 1..450
 /organism="Gallus gallus"
 /db_xref="taxon:9031"
 CDS 1..450
 /note="calmodulin"
 /codon_start=1
 /protein_id="AA048650.1"
 /db_xref="GI:211386"
 /translation="MADQLTEQIAEFKFAFLDKDGDGTTTKELGTVMSLGQNP
 TEAELODMINEVDANGTIDPEFLTMARKKQDSEIEAREARVFDKQNGYIS
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BASE COUNT 160 a 62 c 122 g 106 t
 ORIGIN

Alignment Scores:

Pred. No.: 7.3e-23 Length: 450
 Score: 384.50 Matches: 76
 Percent Similarity: 73.97% Conservative: 32
 Best Local Similarity: 52.05% Mismatches: 35
 Query Match: 52.74% Indels: 3
 DB: 5 Gaps: 2

US-10-031-403-1 (1-146) x CHKCALMA (1-450)

QY 1 MetAlaGlyLeuThrProGluGluGluAlaGlnTyrLysLysAlaPheSerAlaVal 20
 Db 1 ATGGCAGATCAATTAACAGAGAAAGATGCGTAATTCAGAAAGAGCTTTCTCCCTATT 60
 QY 21 AspThrAspGlyAsnGlyThrIleAsnAlaGlnGluLeuGlyAlaAlaLeuLysAlaThr 40
 Db 61 GACAGAGATGGTGTACTACTATTAACAAGAGAGTGGGACTGATGAGATCACTT 120
 QY 41 GlyLysAsnLeuSerGluAlaGlnLeuArgLysLeuIleSerGluValAspSerAspGly 60
 Db 121 GGTGACAGAACCCACAGAGAGATTAACAGACATTCATGAATGAAGATGCGATGAGC 180
 QY 61 AspGlyLeuIleSerPheGlnGluPheLeuThr---AlaAlaArgLysAlaArg----- 77
 Db 181 AATGGCACAATGCTCCAGAGTCTCTGATGATGCTAGAAAAAATGAAGAAATGATACA 240
 QY 78 AlaGlyLeuGluAspLeuGlnValAlaPheArgAlaPheAspGlnAspGlyAspGlyHis 97
 Db 241 GATAGCGAAGAAGAAATTAAGAGAGCTTCGCTGTTTGCACAAGATGGTAATGATTAC 300
 QY 98 IleThrValAspGluLeuArgArgAlaMetAlaGlyLeuGlnProLeuProGlnGlu 117
 Db 301 ATTAGTCTCGCAGAACTTCATGATGATGATCAAAATCTTGGGGAGAGATTAACAGATGAA 360
 QY 118 GluLeuAspAlaMetIleArgGluAlaAspValAspGlnAspGlyArgValAspTyrGlu 137
 Db 361 GAAGTATGATAAAGATTAAGAGAGAGATATGATGATGATGATCAAGTAACTATGAA 420
 QY 138 GluPheAlaArgMetLeu 143
 Db 421 GAGTTTCTACAGATGATG 438

9223 9322: gap of unknown length
9323 10515: contig of 1193 bp in length
10516 10615: gap of unknown length
10616 12083: contig of 1468 bp in length
12084 12183: gap of unknown length
12184 13278: contig of 1095 bp in length
13279 13378: gap of unknown length
13379 14561: contig of 1183 bp in length
14562 15688: contig of 1027 bp in length
15689 15788: gap of unknown length
15789 16987: contig of 1199 bp in length
16988 17087: gap of unknown length
17088 18405: contig of 1318 bp in length
18406 18505: gap of unknown length
18506 19606: contig of 1101 bp in length
19607 19706: gap of unknown length
19707 20952: contig of 1246 bp in length
20953 21052: gap of unknown length
21053 22343: contig of 1291 bp in length
22344 24043: gap of unknown length
24044 24143: contig of 1600 bp in length
24144 25452: gap of unknown length
25453 25552: gap of unknown length
25553 27270: contig of 1718 bp in length
27271 27370: gap of unknown length
27371 28818: contig of 1448 bp in length
28819 28918: gap of unknown length
28919 30073: contig of 1155 bp in length
30074 30173: gap of unknown length
30174 32419: contig of 2246 bp in length
32420 32519: gap of unknown length
32520 33854: contig of 1335 bp in length
33855 33954: gap of unknown length
33955 35233: contig of 1279 bp in length
35234 35333: gap of unknown length
35334 36718: contig of 1385 bp in length
36719 36818: gap of unknown length
36819 38567: contig of 1749 bp in length
38568 40606: gap of unknown length
40607 40706: gap of unknown length
40707 42121: contig of 1415 bp in length
42122 42221: gap of unknown length
42222 43495: contig of 1274 bp in length
43496 43595: gap of unknown length
43596 45157: contig of 1562 bp in length
45158 45257: gap of unknown length
45258 46362: contig of 1105 bp in length
46363 46462: gap of unknown length
46463 47699: contig of 1237 bp in length
47700 47799: gap of unknown length
47800 49856: contig of 2057 bp in length
49857 49956: gap of unknown length
49957 51438: contig of 1482 bp in length
51439 51538: gap of unknown length
51539 53339: contig of 1701 bp in length
53340 53339: gap of unknown length
53340 55126: contig of 1787 bp in length
55127 55226: gap of unknown length
55227 56884: contig of 1658 bp in length
56885 56984: gap of unknown length
56985 58782: contig of 1798 bp in length
58783 58882: gap of unknown length
58883 60529: contig of 1647 bp in length
60530 60629: gap of unknown length
60630 62748: contig of 2119 bp in length
62749 62848: gap of unknown length
62849 64502: contig of 1654 bp in length
64503 64602: gap of unknown length
64603 66492: contig of 1890 bp in length
66493 66592: gap of unknown length

66593 68896: contig of 2304 bp in length
68897 68996: gap of unknown length
68997 71271: contig of 2275 bp in length
71272 71371: gap of unknown length
71372 72552: contig of 1181 bp in length
72553 72652: gap of unknown length
72653 74919: contig of 2267 bp in length
74920 75019: gap of unknown length
75020 76630: contig of 1611 bp in length
76631 76730: gap of unknown length
76731 79024: contig of 2294 bp in length
79025 79124: gap of unknown length
79125 82069: contig of 2945 bp in length
82070 82169: gap of unknown length
82170 84926: contig of 2757 bp in length
84927 85026: gap of unknown length
85027 87577: contig of 2551 bp in length
87578 87677: gap of unknown length
87678 90185: contig of 2508 bp in length
90186 90285: gap of unknown length
90286 93377: contig of 2992 bp in length

Alignment Scores:

Pred. No.: 1,1e-20 Length: 106359
Score: 388.50 Matches: 76
Percent Similarity: 71.43% Conservative: 29
Best Local Similarity: 51.70% Mismatches: 41
Query Match: 53.29% Indels: 1
DB: Gaps: 1

US-10-031-403-1 (1-146) x AC103443 (1-106359)

QY 1 MetalaglyluLeuThrProGluGluAlaGlnTyrLysLysAlaPheSerAlaVal 20
DB 83200 ATGTCACAGCGGTACTACTAAGAGCAGCGCGCTGATTCACCAAGCTTCATAGCGTT 83141
QY 21 AspThrAspGlyAsnGlyThrIleAsnAlaGlnGluLeuGlyAlaAlaLeuLysAlaThr 40
DB 83140 GACAAGAAATAGAGTGGCGGTATCAACGTCACGAGAACTTGAGACGTAATGAGCAGATG 83081
QY 41 GlyLysAsnLeuSerGluAlaGlnLeuArgLysLeuIleSerGluValAspSerAspGly 60
DB 83080 GGTAGAGAACATCCAGAGAGAGAGACCTGAAAGCTCATCTATCCAGGATACACAGATGCG 83021
QY 61 AspGlyGluIleSerPheGlnGluPheLeuThrAlaAlaArgLysAlaArgAlaGly 79
DB 83020 GATGGACCATTAAGCTTTAAGATTCCTGACCGCATGAGAGATTAAGAAAGGAGC 82961
QY 80 LeuGluAspLeuGlnValAlaPheArgAlaPheAspGlnAspGlyAspGlyHisIleThr 99
DB 82960 AAGGAGAGACCTCAGAGCTGTCTCCGCGCTTGTGACCAAGATGATGATGATCATCAGC 82901
QY 100 ValAspGluLeuArgAlaArgAlaMetAlaGlyLeuGlnProLeuProGlnGluGluLeu 119
DB 82900 ATGAGAGAACTCAAGCAAGAGCTGTGTCCAGATGGGAGACCTGTCCAGAGAGAGCTG 82841
QY 120 AspaAlaMetIleArgGlnAlaAspValAlaAspGlnAspGlyArgValAsnTyrGluGluPhe 139
DB 82840 AATGACATCATCGCTGTGCTGATGACACCAAGATGGAAGTGAACATATGAGAGCTTT 82781
QY 140 AlaArgMetLeuAlaGlnGlu 146
DB 82780 CTGAGAGTCTTCCTCGAGAG 82760
RESULT 6
E02314
LOCUS E02314 447 bp RNA linear PAT 29-SEP-1997
DEFINITION DNA encoding calmodulin.
ACCESSION E02314
VERSION E02314.1 GI:2170550
KEYWORDS JP 1990092286-A/1.
SOURCE Rattus norvegicus.
ORGANISM Rattus norvegicus


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OY 141 ArgmetleuAlaIngInu 146
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Db 534 AGGATGCTGCCCGAGAG 551

RESULT 3
AX399961
LOCUS AX399961 913 bp DNA linear PAT 06-JUN-2002
DEFINITION Sequence 132 from Patent WO0218424.
ACCESSION AX399961
VERSION AX399961.1 GI:21336273
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
1
AUTHORS Tang, Y.T., Asundi, V., Zhou, P., Xue, A.J., Ren, F., Zhang, J.,
Wang, J.R., Zhao, Q.A., Wang, D., Liu, C., Dmanac, R.T. and Wehrman, T.
TITLE Nucleic acids and polypeptides
JOURNAL Patent: WO 0218424-A 132 07-MAR-2002;
HYSEQ, INC. (US)

FEATURES
source Location/Qualifiers
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/organism="Homo sapiens"
/db_xref="taxon:9606"
162..602
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/translation="MAGELTPEEAOYKKAFSAVDTDGNGTINAQELGALKATGKLN
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BASE COUNT 175 a 279 c 321 g 138 t

ORIGIN
Alignment Scores:
Pred. No.: 6.77e-50 Length: 913
Score: 726.00 Matches: 145
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.328 Mismatches: 0
Query Match: 99.59% Indels: 0
Gaps: 6

US-10-031-403-1 (1-146) x AX399961 (1-913)
OY 1 MetalGlyGluLeuThrProGluGluAlaGlnTyrLysLysAlaPheSerAlaVal 20
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Db 162 ATGGCGGTGAGCTGACTCTCTGAGGAGGAGGCCAGTACAAAAGCCTTCTCCGCGTT 221

OY 21 AspThrAspGlyAsnGlyThrIleAsnAlaGlnGluLeuGlyAlaIleuLysAlaThr 40
|||||
Db 222 GACACGGATGGAAGACGACCATCAATGCCAGACCTGGCGCGCTGAAGGCCACG 281

OY 41 GlyLysAsnLeuSerGluAlaGlnLeuArgLysLeuIleSerGluValAspSerAspGly 60
|||||
Db 282 GGCAGAAACCTCTCGAGAGGCCAGCTAAGGAACATCATCTCCGAGTTGACAGCGC 341

OY 61 AspGlyGluIleSerPheGlnGluPheLeuThrAlaAlaArgLysAlaArgAlaGlyLeu 80
|||||
Db 342 GACGGGGAATCAGCTTCAGAGTCTCGACGCGCGCGAGGAAGGCCAGGCGCGCTG 401

OY 81 GluAspLeuGlnValAlaPheArgAlaPheAspGlnAspGlyHisIleThrVal 100
|||||
Db 402 GAGGACCTGACAGTCCCTCCGCGCTTCGACAGGATGGCGAGGCCACATACCGGTG 461

OY 101 AspGluLeuArgArgAlaMetAlaGlyLeuGlyGlnProLeuProGlnGluGluLeuAsp 120
|||||
Db 462 GACGAGCTCAGCGGCGCATGGGCGGCTGGGCGACCCCTGCGGAGAGGAGCTGGAC 521

OY 121 AlaMetIleArgGluAlaAspValAspGlnAspGlyArgValAsnTyrGlnGluPheAla 140
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Db 522 GCCATGATCCGAGCGCCAGCTGAGACGAGCGCGGTGAATCAAGAGATTCCGC 581
OY 141 ArgmetleuAlaIngInu 146
|||||
Db 582 AGGATGCTGCCCGAGAG 599

RESULT 4
AL732437
LOCUS AL732437 185926 bp DNA linear HTG 16-AUG-2002
DEFINITION Homo sapiens chromosome 10 clone RP11-116G8, *** SEQUENCING IN
PROGRESS *** 2 unordered pieces.
ACCESSION AL732437.11 GI:22316190
VERSION AL732437
HTG: HTGS_PHASE1; HTGS_ACTIVEFIN; HTGS_DRAFT; HTGS_FULLTOP.
KEYWORDS human.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
1
AUTHORS Bird, C.
TITLE Direct Submission
JOURNAL Submitted (15-AUG-2002) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquerry@sanger.ac.uk Clone requests: clonerequests@sanger.ac.uk
On Aug 19, 2002 this sequence version replaced gi:2204501.

COMMENT
----- Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquerry@sanger.ac.uk
----- Project Information
Center project name: bA116G8
----- Summary Statistics
Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; L08752; 100% of reads
Chemistry: Dye-terminator; 100% of reads
Consensus quality: 185460 bases at least Q40
Consensus quality: 185618 bases at least Q30
Consensus quality: 185788 bases at least Q20
Insert size: 185826; sum-of-contigs
Insert size: 180559; 9.4% error; agarose-ff
Quality coverage: 13.28x in Q20 bases; sum-of-contigs quality
coverage: 14.38x in Q20 bases; agarose-ff
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* NOTE: This is a 'working draft' sequence. It currently
* consists of 2 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 183441: contig of 183441 bp in length
* 183442 183541: gap of 100 bp
* 183542 185926: contig of 2385 bp in length.
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/clone_11b="RPC1-11.1"
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ORIGIN
Alignment Scores:
Pred. No.: 1.83e-47 Length: 185926
Score: 726.00 Matches: 145
Percent Similarity: 100.00% Conservative: 1

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AX077138 858 bp DNA linear PAT 22-FEB-2001
 LOCUS AX077138 Sequence 2 from Patent WO0107604.
 DEFINITION AX077138 GI:13121753
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE
 1 (bases 1 to 858)
 AUTHORS Mehul,B., Bernard,D., and Simonetti,L.
 TITLE Isolated peptide of the horny layer and use thereof
 JOURNAL Patent: WO 0107604-A 2 01-FEB-2001;
 L'OREAL (FR)
 FEATURES
 source location/Qualifiers
 1..858
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 BASE COUNT 155 a 267 c 301 g 135 t
 ORIGIN
 Alignment Scores:
 Pred. No.: 3.65e-50 Length: 858
 Score: 729.00 Matches: 146
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 6 gaps: 0
 US-10-031-403-1 (1-146) x AX077138 (1-858)
 QY 1 MetAlaGlyIuLeuThrProGluGluGluAlaGlnTyrLysLysAlaPheSerAlaVal 20
 Db 114 ATGGCCGGTGGAGTGCCTCTGAGAGAGAGCCAGTACAAAGGCTTCTCGCGGT 173
 QY 21 AspThrAspGlyAsnGlyThrIleAsnAlaGlnIuLeuGlyAlaAlaLeuLysAlaThr 40
 Db 174 GACACGGATGGAAAGCGCACCATCAATGCCAGAGCTGGCGCGGCTGAAAGCCAGC 233
 QY 41 GlyLysAsnLeuSerGluAlaGlnLeuArgLysLeuIleSerGluValAspSerAspGly 60
 Db 234 GGCAAGAACCTCTCGAGGCGCCACCTAAGAACTCATCTCGAGTTGACAGCAGCGCC 293
 QY 61 AspGlyIuIleSerPheGlnGluPheLeuThrAlaAlaArgLysAlaArgAlaGlyLeu 80
 Db 294 GACGGCAAAATCACCTTCCAGAGAGTCTCTGACGGCGGCAAGAGCCAGCGCGCTG 353
 QY 81 GluAspLeuGlnValAlaPheArgAlaPheAspGlnAspGlyAspGlyHisIleThrVal 100
 Db 354 GAGGACCTGCAGGTGCGCTTCCGCGCTTGCACAGAGATGGCGAGCCACATCACCCTG 413
 QY 101 AspGluLeuArgArgAlaMetAlaGlyLeuGlyGlnProLeuProGlnGluGluLeuAsp 120
 Db 414 GACAGAGCTCAGGCGGCGCATGCGCGGCTGGCGAGCGCGTCCGCGAGAGAGACTGGAC 473
 QY 121 AlaMetIleArgGluAlaAspValAspGlnAspGlyArgValAsnTyrGluGluPheAla 140
 Db 474 GCCATGATCCGCGGCGGCGAGCTGACAGACAGCGGCGGTGAACCTACGAGAGCTTCGCG 533
 QY 141 ArgMetLeuAlaGlnGlu 146
 Db 534 AGGATGCTCGCCCGAGAG 551
 RESULT 2
 AF172852 858 bp mRNA linear PRI 01-MAY-2000
 LOCUS AF172852 Homo sapiens calmodulin-like skin protein (CLSP) mRNA, complete
 DEFINITION
 cds
 ACCESSION AF172852
 VERSION AF172852.1 GI:7673315
 KEYWORDS
 SOURCE Homo sapiens.

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE
 1 (bases 1 to 858)
 AUTHORS Mehul,B., Bernard,D., Simonetti,L., Bernard,M.A. and Schmidt,R.
 TITLE Identification and cloning of a new calmodulin-like protein from
 human epidermis
 JOURNAL J. Biol. Chem. 275 (17), 12841-12847 (2000)
 MEDLINE 20239936
 PUBMED 10777582
 REFERENCE
 2 (bases 1 to 858)
 AUTHORS Mehul,B., Bernard,D., Simonetti,L. and Schmidt,R.
 TITLE Direct Submission.
 JOURNAL Submitted (27-JUL-1999) Life Science Research, L'oreal, 90 rue du
 general Roquet, Clichy 92583, France
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 source location/Qualifiers
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 /db_xref="taxon:9606"
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 /tissue_type="skin"
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 BASE COUNT 155 a 267 c 301 g 135 t
 ORIGIN
 Alignment Scores:
 Pred. No.: 3.65e-50 Length: 858
 Score: 729.00 Matches: 146
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 9 gaps: 0
 US-10-031-403-1 (1-146) x AF172852 (1-858)
 QY 1 MetAlaGlyIuLeuThrProGluGluGluAlaGlnTyrLysLysAlaPheSerAlaVal 20
 Db 114 ATGGCCGGTGGAGTGCCTCTGAGAGAGAGCCAGTACAAAGGCTTCTCGCGGT 173
 QY 21 AspThrAspGlyAsnGlyThrIleAsnAlaGlnIuLeuGlyAlaAlaLeuLysAlaThr 40
 Db 174 GACACGGATGGAAAGCGCACCATCAATGCCAGAGCTGGCGCGGCTGAAAGCCAGC 233
 QY 41 GlyLysAsnLeuSerGluAlaGlnLeuArgLysLeuIleSerGluValAspSerAspGly 60
 Db 234 GGCAAGAACCTCTCGAGGCGCCACCTAAGAACTCATCTCGAGTTGACAGCAGCGCC 293
 QY 61 AspGlyIuIleSerPheGlnGluPheLeuThrAlaAlaArgLysAlaArgAlaGlyLeu 80
 Db 294 GACGGCAAAATCACCTTCCAGAGAGTCTCTGACGGCGGCAAGAGCCAGCGCGCTG 353
 QY 81 GluAspLeuGlnValAlaPheArgAlaPheAspGlnAspGlyAspGlyHisIleThrVal 100
 Db 354 GAGGACCTGCAGGTGCGCTTCCGCGCTTGCACAGAGATGGCGAGCCACATCACCCTG 413
 QY 101 AspGluLeuArgArgAlaMetAlaGlyLeuGlyGlnProLeuProGlnGluGluLeuAsp 120
 Db 414 GACAGAGCTCAGGCGGCGCATGCGCGGCTGGCGAGCGCGTCCGCGAGAGAGACTGGAC 473
 QY 121 AlaMetIleArgGluAlaAspValAspGlnAspGlyArgValAsnTyrGluGluPheAla 140
 Db 474 GCCATGATCCGCGGCGGCGAGCTGACAGACAGCGGCGGTGAACCTACGAGAGCTTCGCG 533

GenCore version 5.1.4.p5_4578
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OM protein - nucleic search, using frame_plus_p2n model

Run on: May 16, 2003, 02:38:12 ; Search time 2428 Seconds
(without alignments)
1750.004 Million cell updates/sec

Title: US-10-031-403-1

Sequence: 1 MAGELTPEEEAQQYKKAFAV.....DVDQDGRVNEEFARMLAGE 146

Scoring table:

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-DB=GenEmbl -QFMT=fastap -SUFFIX=rgc -MINMATCH=0.1 -LOOPTCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blomsum62 -TRANS=human40.cdi -LIST=45
-DOCCALIG=200 -THR.SCORE=Pct -THR.MAX=100 -THR.MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=2000000000
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-WARN_TIMEROUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-FGAPOP=10 -YGAPEXT=0.5 -DELop=6 -DELEXT=7

Database :
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3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_da:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*

29: em_vl:*
30: em_hg_hum:*
31: em_hg_in:*
32: em_hg_other:*
33: em_hg_mus:*
34: em_hg_pin:*
35: em_hg_rod:*
36: em_hg_mam:*
37: em_hg_yrt:*
38: em_sy:*
39: em_hggo_hum:*
40: em_hggo_mus:*
41: em_hggo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	729	100.0	858	6	AX077138 Sequence
2	729	100.0	858	9	AF172852 Homo sapi
3	726	99.6	913	6	AX399961 Sequence
4	726	99.6	185926	2	AL732437 Homo sapi
5	388.5	53.3	106359	2	AC103443 Rattus no
6	384.5	52.7	447	6	E02314 DNA encodin
7	384.5	52.7	450	5	CHRCALMA
8	384.5	52.7	476	6	E09262
9	384.5	52.7	476	5	DURCA
10	384.5	52.7	485	6	AX396241
11	384.5	52.7	595	12	SYNARCAL
12	384.5	52.7	599	10	RATCAM
13	384.5	52.7	622	4	AY046946
14	384.5	52.7	654	6	AX401676
15	384.5	52.7	654	6	E02315
16	384.5	52.7	691	10	RSPRCM4
17	384.5	52.7	722	10	MUSCALMDA
18	384.5	52.7	750	5	XELCAM
19	384.5	52.7	799	9	HUMCALCBP
20	384.5	52.7	812	5	XELCAM
21	384.5	52.7	1037	9	BC008597
22	384.5	52.7	1044	10	MUSCAM
23	384.5	52.7	1058	9	BC000454
24	384.5	52.7	1084	10	RATCAM
25	384.5	52.7	1112	10	RATCAM
26	384.5	52.7	1126	9	HUMCAM
27	384.5	52.7	1128	9	HUMALDN
28	384.5	52.7	1131	6	A31920
29	384.5	52.7	1133	9	BC006464
30	384.5	52.7	1134	9	BC003354
31	384.5	52.7	1158	9	BC026055
32	384.5	52.7	1161	9	BC018677
33	384.5	52.7	1163	9	BC017385
34	384.5	52.7	1164	9	BC008437
35	384.5	52.7	1201	10	BC021347
36	384.5	52.7	1361	6	AX305360
37	384.5	52.7	1361	10	MMCALMOD
38	384.5	52.7	1446	10	RNRCLM
39	384.5	52.7	1571	9	BC011834
40	384.5	52.7	1644	5	AF085250
41	384.5	52.7	2175	9	HUMCAM
42	384.5	52.7	2190	9	BC005137
43	384.5	52.7	3513	10	AF178845
44	383.5	52.6	848	3	AB063181
45	382.5	52.5	450	5	ELCCALMA

ALIGNMENTS

RESULT 1